

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2001, 18:21:27 ; Search time 94.78 Seconds

(without alignments)  
6924.896 Million cell updates/sec

Title: US-09-719-272-1

Sequence: 1 gatcgcagctgaagatcc.....attgataatcagattctc 3467

Scoring table:

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Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued\_Patents\_NA:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1285	37.1	6000	1 US-08-348-006B-6	Sequence 6, Appl
2	1285	37.1	6000	2 US-08-800-825A-6	Sequence 6, Appl
3	1285	37.1	6000	4 US-09-158-657-6	Sequence 6, Appl
4	1285	37.1	6000	5 PCT-US94-10166-6	Sequence 6, Appl
5	1273.2	36.7	5690	2 US-08-447-464-2	Sequence 2, Appl
6	1273.2	36.7	5690	2 US-08-716-679-2	Sequence 2, Appl
7	552	15.9	2872	1 US-08-015-985-2	Sequence 4, Appl
8	537.4	15.5	2409	1 US-08-015-985-2	Sequence 4, Appl
9	361.8	10.4	5769	2 US-08-652-971-1	Sequence 1, Appl
10	361.8	10.4	5769	2 US-08-991-953A-1	Sequence 1, Appl
11	361.8	10.4	5769	2 US-08-769-399-1	Sequence 1, Appl
12	361.8	10.4	5769	2 US-08-449-644-3	Sequence 3, Appl
13	335.6	9.7	4374	2 US-08-087-244A-3	Sequence 4, Appl
14	335.6	9.7	4374	2 US-08-449-644-4	Sequence 4, Appl
15	308	8.9	4651	2 US-08-015-973-2	Sequence 2, Appl
16	308	8.9	4651	2 US-08-015-973-2	Sequence 2, Appl
17	260.2	7.5	6924	1 US-08-448-164-2	Sequence 1, Appl
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19	245	7.1	4338	1 US-08-446-363-1	Sequence 1, Appl
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21	194.4	5.6	3969	1 US-08-241-853-1	Sequence 1, Appl
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23	189.2	5.5	5117	3 US-08-854-585-1	Sequence 1, Appl
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25	178.6	5.2	2943	2 US-08-548-159-2	Sequence 2, Appl
26	178.6	5.2	2943	2 US-08-548-159-2	Sequence 2, Appl
27	176.8	5.1	5455	1 US-08-342-930-1	Sequence 1, Appl

28	168.4	4.9	1413	2 US-08-239-276-9	Sequence 9, Appl
29	168.4	4.9	1413	2 US-08-468-579B-9	Sequence 9, Appl
30	168.4	4.9	1413	2 US-08-468-579B-9	Sequence 9, Appl
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32	168.4	4.9	3311	2 US-08-468-579B-10	Sequence 10, Appl
33	168.4	4.9	3311	3 US-08-468-579B-10	Sequence 10, Appl
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37	160.6	4.6	5679	1 US-08-201-697-6	Sequence 6, Appl
38	158.4	4.6	2309	2 US-08-036-210-10	Sequence 10, Appl
39	158.4	4.6	2309	2 US-08-036-210-10	Sequence 10, Appl
40	158.4	4.6	2692	1 US-08-449-609-14	Sequence 14, Appl
41	158.4	4.6	2692	2 US-08-449-609-14	Sequence 14, Appl
42	158.4	4.6	3973	1 US-08-036-210-21	Sequence 21, Appl
43	158.4	4.6	3973	2 US-08-449-609-14	Sequence 21, Appl
44	151.4	4.4	2145	1 US-08-202-389-5	Sequence 5, Appl
45	151.4	4.4	2277	3 US-09-358-685-1	Sequence 1, Appl

## ALIGNMENTS

RESULT 1  
US-08-348-006B-6  
Sequence 6, Application US/08348006B  
Patent No. 5658756  
GENERAL INFORMATION:  
APPLICANT: RODAN, GIDEON A.  
APPLICANT: SCHMIDT, AZRIEL  
APPLICANT: RUTLEDGE, SU JANE  
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN.  
TITLE OF INVENTION: TYROSINE PHOSPHATASE  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: J. MARK HAND  
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000  
CITY: RAHWAY  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/348,006B  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/122,032  
FILING DATE: 14-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: HAND, J., MARK  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 189921A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-594-3905  
TELEFAX: 908-594-4720  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6000 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-348-006B-6

Query Match 37.18; Score 1285; DB 1; Length 6000;  
Best Local Similarity 81.48; Pred. No. 0;  
Matches 1489; Conservative 0; Mismatches 340; Indels 0; Gaps 0;

OY 29 ccaactctctgacccctgtgagatgcygaagcctcaactacagaccaccaagatgacgaga 88  
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 OY 89 ccacacccatcccatcccatcccatcccatcccatcccatcccatcccatcccatcccatcc 4017  
 DB 4018 CCACCCCAATTCCTCCATCCCAATGCGAGCAGACAGGAGCGGCTCAAGGCCAAGCA 4077  
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 DB 4138 AACTTCACACCTTGAGAGTGAACACCCGAAACCGCTATGCCAACGCTATGCCCTATGA 4197  
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 DB 4378 GATGACGCGCTGAG 4437  
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 DB 4498 CTGCGCTCAGAGACATCT 4557  
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 DB 5038 CCGCTGTGTGAACATCATGCTTATGAGAGACACAGGGTGTGTGTCTGCAACCCATCCGGG 5097  
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 OY 1829 actacgcctccctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 1857  
 DB 5758 AAGCCATGCTCCCGCCAGCG 5786

RESULT 2  
 US-08-800-825A-6  
 : Sequence 6, Application US/08800825A  
 : Patent No. 5866397  
 : GENERAL INFORMATION:  
 : APPLICANT: RODAN, GIDEON A.  
 : APPLICANT: SCHMIDT, AZRIEL  
 : APPLICANT: RUTLEDGE, SU JANE  
 : TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN  
 : NUMBER OF SEQUENCES: 7  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: J. MARK HAND - MERCK & CO., INC.  
 : STREET: 126 E. LINCOLN AVE., P.O. BOX 2000  
 : CITY: RAHWAY  
 : STATE: NEW JERSEY  
 : COUNTRY: USA  
 : ZIP: 07065-0900  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800, 825A  
FILING DATE: 14-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HAND, J. MARK  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 18992DA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-3905  
TELEFAX: 732-594-4720  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6000 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-800-825A-6

Query Match 37.1%; Score 1285; DB 2; Length 6000;  
Best Local Similarity 81.4%; Pred. No. 0;  
Matches 1489; Conservative 0; Mismatches 340; Indels 0; Gaps 0;

Oy 29 ccaactccttgagccctgtgagatgagagctcaaccagagcccccagatgacgaga 88  
Db 3958 CCACCCCAAGAGACCTGTGGAATGAGACGATTAATCTCCAGACTCCAGGACTGTAG 4017  
Oy 89 ccaaccacacacccac 148  
Db 4018 CCACCCGCAATTCCTCATGCGAGACATGCGGAGACACACAGAGCGGCTCAAGGCCAACA 4077  
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Oy 1049 ctcaagggccac 1108  
Db 4978 CTCCAGGCTCCACACGTCACGCTTATCATGTCATGTCATGTCATGTCATGTCATGTC 5037  
Oy 1109 ccgagctgtgac 1168  
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Oy 1169 tgtgagaggtctgactac 1228  
Db 5098 TGTGAGGCTGTGACTATCAATCAACCCAGCTTCAATGATGCTTCAAGGACGCAAGAGC 5157  
Oy 1229 ctacatagctac 1288  
Db 5158 CTACATGCGGACACAGGCGCTGCGGAGACACGGAACATCTTGCGGCATGCTGTG 5217  
Oy 1289 gtagac 1348  
Db 5218 GAGAACAAATTTGAGAGATGCTGTGATGCTGATGATGATGATGATGATGATGATGATG 5277  
Oy 1349 atgcac 1408  
Db 5278 GTGTACACAGTACTGCGCGGACGCTCTGCGGCTTACCACTACTTGTGTGATGATGC 5337  
Oy 1409 gatgtgagatgac 1468  
Db 5338 GATGCAAAATTAACACATGCTCTGATATCTGCGAGATTCAGTCAACAGATGCCG 5397  
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Db 5398 GATGAGGACAGTCCGCGGACGCTGCGGAGTTCAGATTCACAGACTGCGGAAACAGGCTGT 5457  
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Db 5458 GCCAAATGCGGGAGAGGCTTATCACTTCAATTTGCGCAAGTCAATTAAGTAAAGACA 5517  
Oy 1589 gtttgacagatgtgacctac 1648  
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Oy 1649 gtccatcactctgagatgtctgtgagacacacacacacacacacacacacacacacacac 1708  
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Oy 1709 tcaagacgtgaaagac 1768  
Db 5638 TGAAGGCTGAAGATGTACCAACCGCGCGCATGTGTCAACAGAGATGAGTA 5697  
Oy 1769 tcaagtgtgac 1828

Db 5698 CCAAGTTCGTTACAGGGGCACTGAGTACCTCGAAGCTTGGACATATGCAACCTA 5757  
 QY 1829 actacgctccctctctctccgacccc 1857  
 Db 5758 AAGCCATGCTCCCCCGACGCCGACAC 5786

## RESULT 3

US-09-158-657-6  
 : Sequence 6, Application US/09158657  
 : Patent No. 6214564  
 : GENERAL INFORMATION:  
 : APPLICANT: RODAN, GIDEON A.  
 : APPLICANT: SCHMIDT, AZRIEL  
 : APPLICANT: RUTLEDGE, SU JANEY  
 : TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN  
 : TITLE OF INVENTION: TYROSINE PHOSPHATASE  
 : NUMBER OF SEQUENCES: 7  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: J. MARK HAND - MERCK & CO., INC.  
 : STREET: 126 E. LINCOLN AVE., P.O. BOX 2000  
 : CITY: RAHWAY  
 : STATE: NEW JERSEY  
 : COUNTRY: USA  
 : ZIP: 07065-0900  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patentin Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/09/158,657  
 : FILING DATE:  
 : CLASSIFICATION:  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 08/800,825  
 : FILING DATE: 14-FEB-1997  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: HAND, J. MARK  
 : REGISTRATION NUMBER: 36,545  
 : REFERENCE/DOCKET NUMBER: 18992DA  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 732-594-3905  
 : TELEFAX: 732-594-4720  
 : INFORMATION FOR SEQ. ID NO: 6:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 6000 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: cDNA  
 : US-09-158-657-6

Query Match 37.18; Score 1285; DB 4; Length 6000;  
 Best Local Similarity 81.48; Pred. No. 0;  
 Matches 1489; Conservative 0; Mismatches 340; Indels 0; Gaps 0;

QY 29 ccaacctctgacctgagagatgagagagctcaataccagaccagatgagaga 88  
 Db 3958 CCACCCCAAGACCTCTGGAAATGAGACCATTAATTCCAGATCCAGGCAATGCTTAG 4017  
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 QY 389 cgaagaccatgaggatcttctgagaaatggtgaggaaagcagcagccactgtgtcat 448  
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 Db 4378 GATGACGCGGCTGGAGGAGAAATGACGATCAAGCTGATCAGTATGTCCTCAACAGAGG 4437  
 QY 509 caccgagacctgtgacctatctacagtgaccctgttgacacagttgagctggcacata 568  
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 QY 569 cactgtgcaccttcgacatccacaagatggctcagtgagaaagcgtgagctgtca 628  
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 QY 869 ctacatgtgacag 928  
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 Db 5218 GGAGAACAAATTCAGATCGTGTGATGCTGACCAACTCGGAGATGGCGGAGAA 5277

PCT-US94-10166-6

Sequence b, Application PC/TUS9410166  
GENERAL INFORMATION:  
APPLICANT: RODAN, GIDEON A  
APPLICANT: SCHMIDT, AZRIEL  
APPLICANT: RUTLEDGE, SU JANE  
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASE  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JOHN W. WALLEIN III  
STREET: P. O. BOX 2000, 126 E. LINCOLN AVE.  
CITY: RAHWAY  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/10166  
FILING DATE: 09-SEPT-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/122,032  
FILING DATE: 14-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WALLEIN, JOHN W III  
REGISTRATION NUMBER: 35403  
REFERENCE/DOCKET NUMBER: 18992  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-594-3905  
TELEFAX: 908-594-4720

PCT-US94-10166-6

Query Match	37.18;	Score 1285;	DB 5;	Length 6000;
Best Local Similarity	81.48;			
Matches 1489;	Conservative			

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269 ccactctcagtcataccttaacctatcatgatgcgqctccgganantaaata  
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RESULT 6  
US-08-716-679-2  
Sequence 2, Application US/08716679  
Patient No. 5846800

GENERAL INFORMATION:  
APPLICANT: Schlessinger, Joseph  
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN  
TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennile & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/716,679  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/130,570  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7683-043  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5690 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

12

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OY	90 caaccacccatccccaatccatccagacctgtgagcaacaactctgtaggaccttaagccaagat	149		
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RESULT 7  
US-08-015-985-4  
; Sequence 4, Application US/08015985  
; Patent No. 5538886  
; GENERAL INFORMATION:



Query Match	15.98;	Score 552;	DB 1;	Length 2872;
Best Local Similarly	59.58;	Pred.	No. 1.8e-124;	
Matches 977; Conservative	0.61;			

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CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Dregger, Ginger R.  
REGISTRATION NUMBER: 33,055  
REFERENCE/DOCKET NUMBER: P1033  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 225-3216  
TELEFAX: (415) 952-9881  
TELEX: 910 371-7168  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5769 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

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Db 3903 GGTACGCGCGCGCTGGATGTGGAGAGTGAACATTTGCTGCTGCCCGGATACGAGA 3962
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Db 4140 GGTCTACGACTACGGGGACCTCCATCGTCACTGCAACCACTTAACCACTCACTCACTC 4199
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Db 4260 GGTGGAGTTGTGTCTGTGGACAGCAACAGAGATTGTGTGCTGCTGCTGCTGCTGCA 4319
Oy 1460 ggaatgcgcggatgagcagctcaag-----gacaaatgcgagctcagctcagacag 1513
Db 4320 GAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4379
Oy 1514 gccag---agcagggcgtgcccagacagagagagagctcagctcagctcagctcag 1570
Db 4380 GTCTCTTATGAGACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4439
Oy 1571 gcaataagaccaaagagctgtgacagagatgagcctatcagctcagctcagctcag 1630
Db 4440 GGACAAAGTGGACGACAGAGAGTGG---GGATGGGCGCACCTGCTGCTGCTGCTGCTG 4496
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RESULT 10
US-08-991-258A-1
: Sequence 1, Application US/08991258A
: Patent No. 5928887
: GENERAL INFORMATION:
: APPLICANT: Chevy, J111
: APPLICANT: Lasky, Laurence A.
: TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT, LLP
: STREET: 4 Embardadero Center, Suite 3400
: CITY: San Francisco
: STATE: California
: COUNTRY: United States
: ZIP: 94111
: COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,258A
FILING DATE: 17-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,971
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63478-3/MHD/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5769 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 379..4686
US-08-991-258A-1

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Query Match
Best Local Similarity 10.4%; Score 361.8; DB 2: Length 5769;
Matches 935; Conservative 1; Mismatches 758; Indels 39; Gaps 8;

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Db 3783 CCTGTGTGGGAGACACCATTCCTGCTACAGATTAAGGCGCCACCTACAGGAGATGAT 3842
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Db 3843 CCGCATGTGACCTCAGACCAATTCCTCCAGCTTCGGGAAGAGTTCCACACGCTGAACCTC 3902
Oy 1049 ctccaaagccc-----acaagtcgctcagcagcagcagcagcagcagcagcagcagcagc 3902
Db 3903 GGTACACGCGCGCTGATGTGAGAGATGTAGACATTTGCCCTGCGCCCGGAATTCAGGA 3962
Oy 1103 caagaacgcgctgtgaaacatcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 3962
Db 3963 CAAGAACCGTAGCATGTGATGTGCTCCACCAACACG---CYGCTGCCCTTCCTCATCTC 4019
Oy 1163 cgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4019
Db 4020 CAGTGTATGGGAGACCCCAATTAATCATATCATATCATATCATATCATATCATATCATATCAT 4222
Oy 1223 gaagcgtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 4079
Db 4080 CCCCCCTTCATCTGATGACCTTCGACCCGCTGACAGATGACACCCCGGCTTCGCGGCT 4139
Oy 1283 gctatgagcagcaatccacatcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 4139
Db 4140 GGTATACGATACGCGGTGACCTTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCAT 4342
Oy 1343 gga---gaatgcaacagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 4199
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Oy 1400 tgttgacagcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 4259
Db 4260 GGTGTGAGTTGTGTGTGACACGACAAACGAGATTTGGTGTCCGAGTGTTCGGGTGCA 4319
Oy 1460 ggaatgcccggatgagcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 4319
Db 4320 GAACCTTTTCGCGTGCAGAGGAGGTCACCTGCTGTACGGGACTCTCCAGTTTCTCGCTTG 4379
Oy 1514 gcccag---agcagggcgtcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 4379
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Oy 1571 gcatagagcagaaagcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 4439
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Oy 1631 cgttgagcagcagcagcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 4496
Db 4497 GGGTGGCGGACGACGACCTTGTGCGCCCTGTGCGCTGTGAGATGATGATGATGATGATGAT 4556
Oy 1691 gggcgtgtgacagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 1750

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Db 4557 CAGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4616
Oy 1751 gcaagcagagagcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 4616
Db 4617 GGAGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4669

RESULT 11
US-08-769-399-1
; Sequence 1, Application US/08769399
; Patent No. 5976852
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jili
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd.
; CITY: South San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/769,399
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 225-3216
; TELEFAX: (415) 952-9881
; TELEX: 910 371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5769 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 379..4686
; US-08-769-399-1

Query Match 10.4%; Score 361.8; DB: 2; Length 5769;
Best Local Similarity 54.0%; Pred. No. 3.7e-78;
Matches 935; Conservative 1; Mismatches 758; Indels 39; Gaps 8;
Oy 89 caaccaccatccatccatccatccatccatccatccatccatccatccatccatccatccatcc 148
Db 2958 CCACCTTGACAGTCCAGTGGCTGATCTTTCACAGCACATCAACACATCAACACACACGCA 3017
Oy 149 tggctcaagtcctccagagatgagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 208
Db 3018 GGGCTAGCGCTTCAAGAGAGAGTACGAGACTTCTTGAAGGCTGTGGAGCGCCACCAAGAA 3077
Oy 209 gaattcaagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcg 3077
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Oy 269 ccaactcgtgcatctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 3125
Db 3126 TCGACACCATGTGAACATACACCGATGCTGCGAGACCTGTGATGCTGCGACTATCTCTGC 3185

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OY 329 caactacatcagatggtacccgaagacagatgacctacatcgccagcgagccctgccc 388  
 DB 3186 CAACATACATAGAGGCGCTACACAGAGTCAACACTTCTATACACCTCAAGGCGCAAGCC 3245  
 OY 389 cgaagccatgagcgatcttcctgagaaatggtggaacagcgacagccatggtcat 448  
 DB 3246 TCAGATGATCTACAGATTTCTGCGCATGCTGTGCGAGAACAGTGTGCGAGATCTCAT 3305  
 OY 449 gatgacacgctggaagaaagtcgcggttaaaatgtagctagctagctgagccgctg 508  
 DB 3306 GATCAACCAAGCTGGTAGAGGTGGCGAGGAGTGAATGTCTGCTACTGCGCTG--AGGA 3362  
 OY 509 caccgagacctgtagctcttcctgagtgacctgttggaacagatgagctggaacata 568  
 DB 3363 CTCAGACATGATGTGGACATCAAGATCACGCTGTAAAGACAGACATCGCTGAGTA 3422  
 OY 569 caactgagacacttcgacactcacaagagtgctcagtgagtgagagcgctgagctgca 628  
 DB 3423 TGTGCTCGGACCTTTCCTTGAGGGGAGAGTTCCTACAGCCCGGCAATGAGTCCGCCA 3482  
 OY 629 gtccagatcagctgagcagacacacagatctcctgagtaaccacatccatcctgagc 688  
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 OY 749 cagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcg 808  
 DB 3603 CAGTCAGAGCACTGCGCGACAGCTGCTGATCATCTGCTGATGATGATGATGATGATG 3662  
 OY 809 gaagacgagaaagagcgatgagcatatcgacagctgacatcgatcgatcagaaagaa 868  
 DB 3663 TGAATGTAGGGGGGCGTGGACATTTTACACTGTGTGAAGAACCTCTGTTCCGAGGGG 3722  
 OY 869 ctacatggtgagaaagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcg 928  
 DB 3723 CAACATGATCCAGAGGAGGAGCAATATCTTCATCTCAGATGCAATCTTGGAGCGCTG 3782  
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 DB 3783 CCTGTGCGGAGAGACACACATCTCTGCAAGATTCAGGCGCACCTTACAGGAGATGAT 3842  
 OY 989 ccaagtgctcagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcg 1048  
 DB 3843 CCGCATTTGACCTTACAGCAATTTCTCCAGCTTTCGGGAAGATTCACAGCTGTAACCTC 3902  
 OY 1049 ctccaagggccc-----acacgctcccgcttcacagcgacacacacacacacacac 1102  
 DB 3903 GGTACACCCCGCTGATGTGAGAGATGTGAGATGCTGCTGCTGCTGCTGCTGCTGCTG 1162  
 OY 1103 caaagacgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 1162  
 DB 3963 CAGAAACCGTAGATGATGTGCTGCTGACACACGCG--CYGCGTGGCTTCTCATCTC 4019  
 OY 1163 cagtggtgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 1222  
 DB 4020 CAGTGTGAGGAGCCCAATAATACATCATCATCATCATCATCATCATCATCATCATCAT 4079  
 OY 1223 gaagcgctacatcagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 1282  
 DB 4080 CCGCGCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4139  
 OY 1283 gctatgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 1342  
 DB 4140 GGTCTACAGCTAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4199  
 OY 1343 gga---gaatgacacagctgacgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 1399  
 DB 4200 GCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4259

OY 1400 ttgtgaccgagtgctgagtaacacatgcccagatatactgctgagtgagtgagtgagc 1459  
 DB 4260 GGTGAGATTGTGTGTGGCCACAGCAAGAGATTTGTGTGTGTGTGTGTGTGTGTGTGTGT 4319  
 OY 1460 ggaatccggagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1513  
 DB 4320 GAACTTTCTGCGGTGAGAGAGGTACCTGCTGTGATGAGCACTTCTGCTGCTGCTGCTG 4379  
 OY 1514 ggcag---agcagggcgatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1570  
 DB 4380 GTCTGCTTATGCGGACAGCGCTGATCTCAGGAAGAGCTTTCGACACTTGTGCTGAGCT 4439  
 OY 1571 gcatagaccag 1630  
 DB 4440 GGAACAGTGCGAGCGAGAGAGTGG---GGATGGCGCACCGGTGTGCTGCTGCAACGG 4496  
 OY 1631 cgtgagcgagcgaggggtgtatcactctgagctgctgctgagcgagcgagcgagcgag 1690  
 DB 4497 GGTGCGCGCGACGTGGACCTTCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCTGCA 4556  
 OY 1691 ggtggtgagcagatggttgcagcgagtgagagagagagagagagagagagagagagagag 1750  
 DB 4557 CAGCGGTGAGATGTTTCTTGTGCTGCGCAAAACATTCGGAACATCAACCAATATGCT 4616  
 OY 1751 gcaagcag 1803  
 DB 4617 GGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4669

RESULT 12  
 US-08-991-953A-1  
 : Sequence 1, Application US/08991953A  
 : Patent No. 6083748  
 : GENERAL INFORMATION:  
 : APPLICANT: Cheng, Jili  
 : TITLE OF INVENTION: A NOVEL KAPPA/MU-LINE PROTEIN TYROSINE  
 : TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
 : NUMBER OF SEQUENCES: 10  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: FLHER, HOBBACH, TEST, ALBRITTON & HERBERT, LLP  
 : STREET: 4 Embarcadero Center, Suite 3400  
 : CITY: San Francisco  
 : STATE: California  
 : COUNTRY: United States  
 : ZIP: 94111  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patent Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/991,953A  
 : FILING DATE: 16-DEC-1997  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/652,971  
 : FILING DATE: 24-MAY-1996  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Dreger, Walter H.  
 : REGISTRATION NUMBER: 24,190  
 : REFERENCE/DOCKET NUMBER: A-63478-3/RHD/MTK  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (415) 781-1989  
 : TELEFAX: (415) 398-3249  
 : TELEX:  
 : INFORMATION FOR SEQ ID NO: 1:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 5769 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: DNA (genomic)



[illegible][illegible]



US-08-087-244A-3  
Sequence 3, Application US/08087244A  
Patent No. 5863755

GENERAL INFORMATION:  
APPLICANT: Schlesinger, Joseph  
APPLICANT: Sap, Jan M.  
APPLICANT: Ulrich, Axel  
APPLICANT: Vogel, Wolfgang  
APPLICANT: Fuchs, Miriam  
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHORYROSINE  
TITLE OF INVENTION: PHOSPHATASE-KAPPA  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
CITY: New York  
STREET: 1155 Avenue of the Americas  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATE:  
APPLICATION NUMBER: US/08/087,244A  
FILING DATE: 01-JUL-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/POCKET NUMBER: 7683-042  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8664/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4374 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..4371  
08-087-244A-3

[illegible][illegible]

Oy 1266 gagactctctgagcagctatgagagacaaattccacatcatcagctcagctaccag 1325  
 Db 3820 AAAGACTCTCGAGATTACTATATGATACGATGATACCTCATCTGATGATTAATGAA 3879  
 Oy 1326 ctccggagatgagcagaggaatgcccacagctcagcagcagcagcagcagcagcag 3879  
 Db 3880 GTGGACCTCTC-----AGGGCTGCCACAGTACGCGCCAGAACAGAAATGCTGGCA 3933  
 Oy 1386 taccagtaacttctgtgtgaccagatgct-----gagtaacaatgcccagat 1436  
 Db 3934 TATGCTCTTATCAAGTGAATGATATCTTTTCAATGACCTGATGATCTATCAATGCA 3993  
 Oy 1437 atccggcgtgctcagagctcagcagcagcagcagcagcagcagcagcagcagcagcag 1496  
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 Oy 1497 ttccagltcacagactgagcagagcagcagcagcagcagcagcagcagcagcagcag 1556  
 Db 4054 CAGTACTAGGCTGGGCTTCTCATGAGAAAGTGCCTGCTCAAAAGCTGTTTGGAA 4113  
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 Oy 1674 gagcagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1733  
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 Oy 1734 cagcctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1793  
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 Oy 1794 gagactctg 1803  
 Db 4354 GAGTACTGG 4363

RESULT 15  
 US-08-449-644-4  
 Sequence 4, Application US/08449644  
 Patent No. 5856162  
 GENERAL INFORMATION:  
 APPLICANT: Schlessler, Joseph  
 APPLICANT: Sap, Jan M.  
 APPLICANT: Ollrich, Axel  
 APPLICANT: Vogel, Wolfgang  
 APPLICANT: Fuchs, Miriam  
 TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHORYROSINE  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PENNIE & EDMONDS  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/449,644  
 FILING DATE: 24-MAY-1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/087,244

FILING DATE: 01-JUL-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7683-042  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-790-9090  
 TELEFAX: 212-869-8864/9741  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4651 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: unknown  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..4317  
 US-08-449-644-4

Query Match 8.98; Score 308; DB 2; Length 4651;  
 Best Local Similarity 51.28; Pred. No. 3.8e-65;

Matches 887; Conservative 0; Mismatches 815; Indels 30; Gaps 6;  
 Oy 90 caccacccatcccatcccatcccatcccatcccatcccatcccatcccatcccatcccatcc 149  
 Db 2590 CATCCAGCATCAGGATGACGATTTTACGACACATTAATCTCATAGACATCAAGAC 2649  
 Oy 150 ggcctcaagcttcccgagctatgagcagcagcagcagcagcagcagcagcagcagcagc 209  
 Db 2650 AGCTATGCTTCAAAAGAGATATGAGACTTTTGAAGGACATGCTGATCTTGGAT 2709  
 Oy 210 aattcaacctgagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2769  
 Db 2710 GTAGCTTAAATGATCAAAATGAGCAAAATGAGCAAAATGAGCAAAATGAGCAAAATG 2829  
 Oy 270 cactctcagctcactcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 329  
 Db 2770 CACTCCAGATGATTTTGCACCCGTAAGAGATGATCTTCTCATGATTAATTAATGCC 2829  
 Oy 330 aactacatgagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 389  
 Db 2830 AACTATATGATGCTTACACAGACCAAGCATTAATGATTAATGATTAATGATTAATG 2889  
 Oy 390 gagacacatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 449  
 Db 2890 GAAACAGTATGATTTCTGAGAGATGATTTGCAAGAAACATCTGCTTCATGATG 2949  
 Oy 450 atgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 509  
 Db 2950 GTTACAAATTTATGATGAGTGGCCCGGTTAAATCTTAATTAATTTGGCTG---ATGAT 3006  
 Oy 510 accgagcctgctgctcattcaggtgacccctgctgagcagcagcagcagcagcagcagc 569  
 Db 3007 ACTGAAGTTTATGCTGACTTCAAAATGATGATGATGATGATGATGATGATGATGATG 3066  
 Oy 570 actgtgacacctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 629  
 Db 3067 GTAGTTAGGACATTCACCTCGAAGAGAGGAGGATGATGATGATGATGATGATGATG 689  
 Oy 630 ttccagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3126  
 Db 3127 TTCAATTTACAGGCTGCTGCTGACATGAGATGCTCCTACCATGCTACAGGCTGCTTCC 3186  
 Oy 690 ttccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 749  
 Db 3187 TTATCCGCGAGTCAAGTATCAAAACCTTCCAGTGTGCCCCCATGCTGTATCATTC 3246  
 Oy 750 agcgggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 809  
 Db 3247 AGTCTGTGCTGACGAACTGCTGTACATTTGATGATGATGATGATGATGATGATGATG 3306

OY 810 aagcagagagaagcggctgacatctatgccaagctgacatgcatcacagaggaaac 869  
Db 3307 GAAGAAGAGGGTGTGTTGATATTACATATTGTGTCAAGCTTAAGATCTCGGCTATT 869  
OY 870 tacatggtgacagagagagcagtaacgtgcatcatalcagagcgctgtagagcgctcc 3366  
Db 3367 AATATGTCACACACAGAGAGAGAGTACATTTTATTCATGATGCCAATTTAGAACCTTGC 3366  
OY 930 acgtgagccacacagagagtgctgtagccgaacctglatgccacatccagaagctgggc 3426  
Db 3427 TTAATGTGGAGAACTGCCATACCTGCTGTGAAATTTAAAGCTGCATATTTGATATGAT 3426  
OY 990 caagtgcctccagaggagagtgtagcccatgagctcgagctcgatcaagctgctg----- 1043  
Db 3487 AGAATAGACTCCAGACTACTCTTATCAATCTCAAGATGAATTCAGACTCTGAATTCA 3486  
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OY 1404 gaccgagtgct-----gagtaacatgccccatatactcgtgtagtcaag 3897  
Db 3898 GAATGATGCTCTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3897  
OY 1455 gtcagagtgccgggagtgtagcagtaagagacatccggcagctcagctcagactg 3957  
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Db 4078 AAGTGCACAGAGAGATGCGAGAGAGAGAGAGAGAGAGAGAGATTTCACTGCTTAATGCT 4077  
OY 1632 gtagggcgacccggggtgtagcactgtagcagctgtagcagcagcagcagcagcag 4137  
Db 4138 GGGGGGCGAG 4137  
OY 1692 ggcgtggtgagacatgtagcagagcgtgtagcagcagcagcagcagcagcagcag 4197  
Db 4198 AATGTTGATGATTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4197  
OY 1752 cagaacagagagcagctacagctgtagcagcgtgtagcagcagcagcagcagcagcag 4257  
Db 4258 GAAGCCCCGAG 4257

71

---

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2001, 18:23:17 : Search time 209.68 Seconds  
(without alignments)  
10382.177 Million cell updates/sec

Title: US-09-719-272-1  
Sequence: 3467  
1 gatccgactgaagacttc.....attgaataatcagattct 3467

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

#### Database :

1: /SIDSB/gcgdata/geneseq/geneseq/NA1980.DAT.\*  
2: /SIDSB/gcgdata/geneseq/geneseq/NA1981.DAT.\*  
3: /SIDSB/gcgdata/geneseq/geneseq/NA1982.DAT.\*  
4: /SIDSB/gcgdata/geneseq/geneseq/NA1983.DAT.\*  
5: /SIDSB/gcgdata/geneseq/geneseq/NA1984.DAT.\*  
6: /SIDSB/gcgdata/geneseq/geneseq/NA1985.DAT.\*  
7: /SIDSB/gcgdata/geneseq/geneseq/NA1986.DAT.\*  
8: /SIDSB/gcgdata/geneseq/geneseq/NA1987.DAT.\*  
9: /SIDSB/gcgdata/geneseq/geneseq/NA1988.DAT.\*  
10: /SIDSB/gcgdata/geneseq/geneseq/NA1989.DAT.\*  
11: /SIDSB/gcgdata/geneseq/geneseq/NA1990.DAT.\*  
12: /SIDSB/gcgdata/geneseq/geneseq/NA1991.DAT.\*  
13: /SIDSB/gcgdata/geneseq/geneseq/NA1992.DAT.\*  
14: /SIDSB/gcgdata/geneseq/geneseq/NA1993.DAT.\*  
15: /SIDSB/gcgdata/geneseq/geneseq/NA1994.DAT.\*  
16: /SIDSB/gcgdata/geneseq/geneseq/NA1995.DAT.\*  
17: /SIDSB/gcgdata/geneseq/geneseq/NA1996.DAT.\*  
18: /SIDSB/gcgdata/geneseq/geneseq/NA1997.DAT.\*  
19: /SIDSB/gcgdata/geneseq/geneseq/NA1998.DAT.\*  
20: /SIDSB/gcgdata/geneseq/geneseq/NA1999.DAT.\*  
21: /SIDSB/gcgdata/geneseq/geneseq/NA2000.DAT.\*  
22: /SIDSB/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3467	100.0	3467	AA291907	Human protein tyro
2	3467	100.0	3467	AA259132	LAR tyrosine phosph
3	3463	99.9	7702	AA88739	Human protein tyro
4	3463	99.9	7702	AA291908	Human protein tyro
5	3463	99.9	7702	AA259133	LAR tyrosine phosph
6	2914.4	84.1	3064	AA259133	Human prostate can
7	1285	37.1	6000	AA086478	Human PTP-OB. Hom
8	1285	37.1	6000	AA086478	Human protein tyro
9	1285	37.1	6000	AA086478	Human protein tyro
10	1273.2	36.7	16	AA086902	Rat receptor type-
11	1059	30.5	16	AA086902	Tyrosine phosphata

12	970	28.0	1029	20	AA24802	Leukocyte antigen
13	578.4	16.7	601	21	AAA44322	Human secreted exp
14	552	15.9	2872	13	AA021001	Murine receptor-ty
15	552	15.9	2872	17	AA736881	Murine receptor-ty
16	552	15.9	2872	20	AA298853	Mouse receptor-ty
17	537.4	15.5	2409	17	AA736882	Mouse receptor-ty
18	537.4	15.5	2409	20	AA298853	Human receptor-ty
19	387.2	11.2	5581	19	AAV17098	Human receptor-ty
20	361.8	10.4	5769	19	AAV15004	Human pancreatic c
21	343	9.9	459	15	AA068707	Receptor protein t
22	329.2	9.5	4574	15	AA068707	Murine protein ty
23	317	9.1	421	15	AA068703	Murine receptor-ty
24	308	8.9	4651	15	AA072914	Murine protein ty
25	306.4	8.8	5775	20	AA072913	Murine receptor-ty
26	260.2	7.5	6924	15	AA068539	Human receptor-ty
27	245	7.1	4338	15	AA067283	Human RPRP-beta.
28	194.4	5.6	3969	19	AA071842	Human RPRP-gamma.
29	194.4	5.6	3969	20	AAV05762	Chicken protein ty
30	190.2	5.5	3669	19	AAV05762	Chicken transmembr
31	188.2	5.5	5117	21	AAV05762	Human protein tyro
32	184.4	5.3	188	21	AAV06027	hudep-1 cDNA. Hom
33	180.2	5.2	1163	18	AA795229	Human ovarian carc
34	180.2	5.2	2464	18	AA795221	Human islet cell a
35	178.6	5.2	2840	18	AA767297	Human islet cell a
36	178.6	5.2	2943	18	AA767295	Type I diabetes-as
37	178.6	5.2	2994	18	AA788478	Human insulinoma-a
38	178.6	5.2	3310	18	AA767296	Human insulinoma-a
39	178.6	5.2	1839	21	AA888655	Type I diabetes-as
40	178.4	5.1	4136	18	AA795222	Mouse vascular-end
41	177	5.1	5455	19	AAV33577	Human protein tyro
42	176.8	5.0	2171	18	AA795222	Osteoclast-tyro
43	172.2	5.0	2736	18	AA795231	Macaque islet cell
44	172.2	5.0	3287	18	AA795231	Macaque islet cell
45	172.2	5.0	3287	18	AA795220	Macaque islet cell

#### ALIGNMENTS

RESULT 1	AA291907	standard: DNA: 3467 BP.
ID	AA291907	
XX	AA291907	
AC	AA291907	
XX	07-JUN-2000 (first entry)	
XX		
DE	Human protein tyrosine phosphatase specific antibody coding sequence.	
XX		
KW	Human: protein tyrosine phosphatase; antibody; intracellular domain; LAR;	
KW	CD45; PTP; diagnosis; insulin resistance related disease; syndrome X;	
KW	non-insulin dependent diabetes mellitus; arteriosclerosis; therapy;	
XX	heart disorder; ss.	
XX		
OS	Homo sapiens.	
XX		
XX	MO200002922-A1.	
XX	20-JAN-2000.	
PD		
XX		
PF	06-JUL-1999: 99MO-JP03656.	
XX		
PR	10-JUL-1998: 98MO-JP03120.	
XX		
PA	(FUSO ) FUSO PHARM IND LTD.	
XX		
PI	Yamamoto H, Tsujikawa K, Uchino Y;	
XX		
DR	WPI: 2000-182215/16.	
DR	P-PSDB: AAV81783.	
XX		
PT	Antibody for diagnosis and treatment of insulin resistance disorders	
PT	and syndrome X recognises the intracellular domains of tyrosine	



Db 1861 cgtgggctccggagggaaccagctctctgaaccataccgacatcgtccagccctcc 1920  
 Oy 1921 taagcagatgctgctcaactgagcagagacagccacgaggatcacagcgttttcaagaagct 1980  
 Db 1921 taagcagatgctgctcaactgagcagagacagccacgaggatcacagcgttttcaagaagct 1980  
 Oy 1981 tgcacacacaaatcagagagagccttagaacaatcccttgagcaagtgtatgtgcccagagcag 2040  
 Db 1981 tgcacacacaaatcagagagagccttagaacaatcccttgagcaagtgtatgtgcccagagcag 2040  
 Oy 2041 cactgtgacctctgtccacacagaccacttgagcccgcttcaaatctctctgtgcg 2100  
 Db 2041 cactgtgacctctgtccacacagaccacttgagcccgcttcaaatctctctgtgcg 2100  
 Oy 2101 tcccgacattctcattgctctctctctgtggggtggggttggggttggggttggggttggggtt 2160  
 Db 2101 tcccgacattctcattgctctctctctgtggggtggggttggggttggggttggggttggggtt 2160  
 Oy 2161 acattaaagtggggtgagacatgagagattttagccctctccctccctccctccctccctccct 2220  
 Db 2161 acattaaagtggggtgagacatgagagattttagccctctccctccctccctccctccctccct 2220  
 Oy 2221 atccggtatctgcagaaatgggacatgtaggggttggggttggggttggggttggggttggggtt 2280  
 Db 2221 atccggtatctgcagaaatgggacatgtaggggttggggttggggttggggttggggttggggtt 2280  
 Oy 2281 tttttttgtatgact 2340  
 Db 2281 tttttttgtatgact 2340  
 Oy 2341 ctgacagcttgagcggaggctcgccgttggcgggagagcagtgctgctccgctccgctccgctcc 2400  
 Db 2341 ctgacagcttgagcggaggctcgccgttggcgggagagcagtgctgctccgctccgctccgctcc 2400  
 Oy 2401 tccagcccttcagagagagct 2460  
 Db 2401 tccagcccttcagagagagct 2460  
 Oy 2461 agtttgttttccctttaaagcctttttagggcacaatgtagcagtggttggcgggagaga 2520  
 Db 2461 agtttgttttccctttaaagcctttttagggcacaatgtagcagtggttggcgggagaga 2520  
 Oy 2521 agataggggaacacatccctctgct 2580  
 Db 2521 agataggggaacacatccctctgct 2580  
 Oy 2581 gaacacagatgctgctgagagagcctgagcagcattccctccatcacacatgctgttgcga 2640  
 Db 2581 gaacacagatgctgctgagagagcctgagcagcattccctccatcacacatgctgttgcga 2640  
 Oy 2641 aaggtttaaatacaaaaaaacaac 2700  
 Db 2641 aaggtttaaatacaaaaaaacaac 2700  
 Oy 2701 aaaaaaatacaaaaaaagaagtcagcccttggttctgtcttcaaacctccaagaaggagaaga 2760  
 Db 2701 aaaaaaatacaaaaaaagaagtcagcccttggttctgtcttcaaacctccaagaaggagaaga 2760  
 Oy 2761 accctgctgctcctgggggttcccgaggagcctgctgctgacacacacacacacacacacacac 2820  
 Db 2761 accctgctgctcctgggggttcccgaggagcctgctgctgacacacacacacacacacacacac 2820  
 Oy 2821 ctttggctccacagatgagtagtgctgctgctgctgctgctgctgctgctgctgctgctgctgct 2880  
 Db 2821 ctttggctccacagatgagtagtgctgctgctgctgctgctgctgctgctgctgctgctgctgct 2880  
 Oy 2881 ggcacagtgagtagacacagtgtaggt 2940  
 Db 2881 ggcacagtgagtagacacagtgtaggt 2940  
 Oy 2941 cgggggctgctgctccttcaggtccaggtccaggtccaggtccaggtccaggtccaggtccaggtcc 3000  
 Db 2941 cgggggctgctgctccttcaggtccaggtccaggtccaggtccaggtccaggtccaggtccaggtcc 3000

Oy 3001 cagagcaggggcccagatgatttctctccctggttctgagcgtgttttcaaaagcccccagta 3060  
 Db 3001 cagagcaggggcccagatgatttctctccctggttctgagcgtgttttcaaaagcccccagta 3060  
 Oy 3061 atcgcctcttccactccacagaatgcctccataaaccaatgtggcagaactactggaattc 3120  
 Db 3061 atcgcctcttccactccacagaatgcctccataaaccaatgtggcagaactactggaattc 3120  
 Oy 3121 tatcaatgtactcaatccacagtcctctatataccagctgtctgaggggagggagagcgc 3180  
 Db 3121 tatcaatgtactcaatccacagtcctctatataccagctgtctgaggggagggagagcgc 3180  
 Oy 3181 ctcttctctctgagcagcgtatctagatagtagtgaggcgggaggggtgcataagct 3240  
 Db 3181 ctcttctctctgagcagcgtatctagatagtagtgaggcgggaggggtgcataagct 3240  
 Oy 3241 gtttagtgaggagcgt 3300  
 Db 3241 gtttagtgaggagcgt 3300  
 Oy 3301 acattccaggtgtgtagtattgt 3360  
 Db 3301 acattccaggtgtgtagtattgt 3360  
 Oy 3361 tgcgtgtagttagttagttagttagttagttagttagttagttagttagttagttagttagttagt 3420  
 Db 3361 tgcgtgtagttagttagttagttagttagttagttagttagttagttagttagttagttagttagt 3420  
 Oy 3421 tcatctcatatctctgtagttagttagttagttagttagttagttagttagttagttagttagttagt 3480  
 Db 3421 tcatctcatatctctgtagttagttagttagttagttagttagttagttagttagttagttagttagt 3480  
 RESULT 2  
 AA259132  
 ID AA259132 standard; DNA; 3467 BP.  
 AC AA259132;  
 XX  
 DT 17-APR-2000 (first entry)  
 XX  
 DE LAR tyrosine phosphatase intracellular domain coding sequence.  
 XX  
 KW Intracellular domain; P-subunit; human; leucocyte antigen related; LAR;  
 XX tyrosine phosphatase; antibody; thyroid cancer; ds.  
 OS Homo sapiens.  
 XX  
 PN M09964591-A1.  
 PM  
 XX  
 PD 16-DEC-1999.  
 XX  
 PF 07-JUN-1999; 99MO-JP03054.  
 XX  
 PR 08-JUN-1998; 98MO-JP02542.  
 XX  
 PA (FUSO ) FUSO PHARM IND LTD.  
 XX  
 PI Yamamoto H, Teujikawa K, Uchino Y, Konishi N;  
 DR WPI: 2000-097539/08.  
 DR P-PSDB: AAY56098.  
 XX  
 PT Antibody recognizing the intracellular domain of the human tyrosine  
 PS phosphatase LAR -  
 XX  
 XX  
 Claim 4: Page 73-78; 104pp; Japanese.  
 This sequence represents the coding region for the intracellular domain  
 (P-subunit) of the human leucocyte antigen related (LAR) tyrosine  
 phosphatase (complete sequence in AA259133). The invention relates to  
 the generation of an antibody recognizing the intracellular domain of

Qy	961	acctgtatgccacatccaaagactctggccaaagtccctccaggggagagtgtgaacgccca	1020
Db	961	accgttatgccacatccaaagactctggccaaagtccctccaggggagagtgtgaacgccca	1020
Qy	1021	tgaagccagaggttcaaagttgtctggccagctccaaagagcccaacgtcccgctctcaacgt	1080
Db	1021	tgaagccagaggttcaaagttgtctggccagctccaaagagcccaacgtcccgctctcaacgt	1080
Qy	1081	ccaacctgcctgcacaacaaagttcaaaaacccgctctgtgaatactatgtccctcaagatga	1140
Db	1081	ccaacctgcctgcacaacaaagttcaaaaacccgctctgtgaatactatgtccctcaagatga	1140
Qy	1141	cccgctgtgtgtctgcagagcccaatccgtgtgtgtgaagagctctgtactatacatatgcagct	1200
Db	1141	cccgctgtgtgtctgcagagcccaatccgtgtgtgtgaagagctctgtactatacatatgcagct	1200
Qy	1201	tctctgtatgttatatagaacagagagagctctcatatagctcaacaaagagagctctcttgacaga	1260
Db	1201	tctctgtatgttatatagaacagagagagctctcatatagctcaacaaagagagagctctcttgacaga	1260
Qy	1261	gaaacagagagatctctgcgcgcatgtctaagggagacaattccacacatcatctgtcatgtga	1320
Db	1261	gaaacagagagatctctgcgcgcatgtctaagggagacaattccacacatcatctgtcatgtga	1320
Qy	1321	ccaagctctcggagagatctggcagaggagaaatgtcccaacgaatctcgtgcagagagagctctg	1380
Db	1321	ccaagctctcggagagatctggcagaggagaaatgtcccaacgaatctcgtgcagagagagctctg	1380
Qy	1381	ctcgcgtaccagtaactgtgtgtgtgaacccaatgtgctgtgatacaacatgtgcccacagtatatcc	1440
Db	1381	ctcgcgtaccagtaactgtgtgtgtgaacccaatgtgctgtgatacaacatgtgcccacagtatatcc	1440
Qy	1441	tgcgtgagatcaaaagttcaacggatgtccggagatgtgcagttcaagagacaatccgcagcttcc	1500
Db	1441	tgcgtgagatcaaaagttcaacggatgtccggagatgtgcagttcaagagacaatccgcagcttcc	1500
Qy	1501	agttcaacagactctgcagagacagagcgtgtgcacaaagacagtcgagagatattcatattgtctcca	1560
Db	1501	agttcaacagactctgcagagacagagcgtgtgcacaaagacagtcgagagatattcatattgtctcca	1560
Qy	1561	tcgggcagagtgatcaataaagacaaagaaacagatttgagacaagataagggctcatatgcagttcca	1620
Db	1561	tcgggcagagtgatcaataaagacaaagaaacagatttgagacaagataagggctcatatgcagttcca	1620
Qy	1621	gcagatgtcgtgcgtgtggccgcacacccggagttctatcaactcttgagacatctgtctcttgagacgca	1680
Db	1621	gcagatgtcgtgcgtgtggccgcacacccggagttctatcaactcttgagacatctgtctcttgagacgca	1680
Qy	1681	tgcgcctatggagggcgtgtgtcgcagatgtttcagaaccgttgaaagaccctgttatcaacagctc	1740
Db	1681	tgcgcctatggagggcgtgtgtcgcagatgtttcagaaccgttgaaagaccctgttatcaacagctc	1740
Qy	1741	ctgcacatctgtgcagagagagagacaggttatcagctgtgttatccgtgtgcggcccttgagttacc	1800
Db	1741	ctgcacatctgtgcagagagagagacaggttatcagctgtgtgttatccgtgtgcggcccttgagttacc	1800
Qy	1801	tcgggcagactcttgacacactatgcgaacgttaactacacgcctccctctccctccgcgcacacccgcg	1860
Db	1801	tcgggcagactcttgacacactatgcgaacgttaactacacgcctccctctccctccgcgcacacccgcg	1860
Qy	1861	cgttgagggtcccgagaggagacccacagctccctctgtgaacatacagagacatctgtccagccctcc	1920
Db	1861	cgttgagggtcccgagaggagacccacagctccctctgtgaacatacagagacatctgtccagccctcc	1920
Qy	1921	tacgcagatgtctgtcaactctgcagagacagaccacacacggggagatccacagctttcaagaaagct	1980
Db	1921	tacgcagatgtctgtcaactctgcagagacagaccacacacggggagatccacagctttcaagaaagct	1980
Qy	1981	tgcacacacaaatcagagagagctctgaacataccctctgggcaagtgagatggccacagacagag	2040
Db	1981	tgcacacacaaatcagagagagctctgaacataccctctgggcaagtgagatggccacacagagag	2040



OY	2041	ccgfygsccttctgttccacaaacccacctvgagcccgcttcaagctctgttcgc	2100
Dp	2041	cactvggcctctctgttccacaaacccacccctvgagcccgcttcaagctctgttcgc	2100
OY	2101	ttccgcattctctactgtctctctccatcvggggtggggtgttggggcaaacctctttaat	2160
Dp	2101	ttccgcattctctactgtctctctccatcvggggtggggtgttggggcaaacctctttaat	2160
OY	2161	acattaaagtgggttagaccggaagatttagcctctctccctgtattttctcttcgga	2220
Dp	2161	acattaaagtgggttagacttagggatttagcctctctccctgtattttctcttcgga	2220
OY	2221	atccgatactcgaanaatvgggccactgttaggggtgttggggtttattttgttttttt	2280
Dp	2221	atccgatactcgaanaatvgggccactgttaggggtgttggggtttattttgttttttt	2280
OY	2281	ttctttttgtatgaactctctgtctgaagaagacgaacatgtcctctccctgtcgaagctggg	2340
Dp	2281	ttctttttgtatgaactctctgtctgaagaagacgaacatgtcctctccctgtcgaagctggg	2340
OY	2341	ctgcacagcccgagccggaagctctggccggtggccgggagcagtgctgaatccggctgc	2400
Dp	2341	ctgcacagcccgagccggaagctctggccggtggccgggagcagtgctgaatccggctgc	2400
OY	2401	ttccagccctctcaagacgaatccctgttttcaactaataatgaagggaacccaatgtttttta	2460
Dp	2401	ttccagccctctcaagacgaatccctgttttcaactaataatgaagggaacccaatgtttttta	2460
OY	2461	agttttgtttctccctttaaagcctttttttaaggccaattgaagaagtgttgggcggggaga	2520
Dp	2461	agttttgtttctccctttaaagcctttttttaaggccaattgaagaagtgttgggcggggaga	2520
OY	2521	agataagggaacacatcaatccctctgtctgtctatacccaatgtgttttaacattcaaccca	2580
Dp	2521	agataagggaacacatcaatccctctgtctgtctatacccaatgtgttttaacattcaaccca	2580
OY	2581	gaaccacgaatgttctctggagaagcctctggcaaggaatctctcatcacaatcgtgtttgga	2640
Dp	2581	gaaccacgaatgttctctggagaagcctctggcaaggaatctctcatcacaatcgtgtttgga	2640
OY	2641	aaggtttaaaaaaacaanaaaccaaaacccaataataaaaaaacaanaaaccaaaaccca	2700
Dp	2641	aaggtttaaaaaaacaanaaaccaaaacccaataataaaaaaacaanaaaccaaaaccca	2700
OY	2701	aaaaaaaaaaaaaaaaaagatcagccctctgtctctgtcttcaaacccctcaagagggaaga	2760
Dp	2701	aaaaaaaaaaaaaaaaaagatcagccctctgtctctgtcttcaaacccctcaagagggaaga	2760
OY	2761	actccgtgtgccttgggggttcccgagggaacctgtcgtcgtacactgggccaagaagcttgg	2820
Dp	2761	actccgtgtgtccttgggggttcccgagggaacctgtcgtcgtacactgggccaagaagcttgg	2820
OY	2821	ctttgttccccaacatctgacagatagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2880
Dp	2821	ctttgttccccaacatctgacagatagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2880
OY	2881	ggccaaagtgtgaatacagaaggttaagggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2940
Dp	2881	ggccaaagtgtgaatacagaaggttaagggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2940
OY	2941	cggggggt	3000
Dp	2941	cggggggt	3000
OY	3001	cagaaacaggggccaagaatatttctctctcgtgtttgtcaagctgttttcaagccccagata	3060
Dp	3001	cagaaacaggggccaagaatatttctctctcgtgtttgtcaagctgttttcaagccccagata	3060
OY	3061	atcgtctcttccaatcccaagatgcccctcaataaaccaatgtgtgtgtgtgtgtgtgtgtgt	3120
Dp	3061	atcgtctcttccaatcccaagatgcccctcaataaaccaatgtgtgtgtgtgtgtgtgtgtgt	3120
OY	3121	tatcaatgttactctcaatcagatctctattatatacccaagcttgcgtgtgtgtgtgtgtgtgtgt	3180

Db	3121	tatcaatgtaactaatcagtccttatatccagcttgctgaggggtaaggaaagcgc	3160
QY	3181	cccttcccttgggcagcgctatctcagatagtgtaagtgggggcggggaggtgcatacgt	3240
Db	3181	cccttcccttgggcagcgctatctcagatagtgtaagtgggggcggggaggtgcatacgt	3240
QY	3241	gttttagcttgaggagcgtgtgtgccgaagatcccaaacctcagctcgaagtcagaagatca	3300
Db	3241	gttttagcttgaggagcgtgtgtgccgaagatcccaaacctcagctcgaagtcagaagatca	3300
QY	3301	acatcccaagggttggtaatcgttggatgatgaacatcatcttttaacctgtgtgaatcag	3360
Db	3301	acatcccaagggttggtaatcgttggatgatgaacatcatcttttaacctgtgtgaatcag	3360
QY	3361	tgccttgtaggttcacgtctgttacaacgctgtttctcatttcttaaganaaacctacgca	3420
Db	3361	tgccttgtaggttcacgtctgttacaacgctgtttctcatttcttaaganaaacctacgca	3420
QY	3421	tcatggcataatctctgtatgtgtaataatttgaataatcagaatttctc	3467
Db	3421	tcatggcataatctctgtatgtgtaataatttgaataatcagaatttctc	3467

### RESULT 3

ID	AAA88739	standard; cDNA; 7702 BP.
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98	98	98
99	99	99
100	100	100

AC AAA88739;

DT 19-FEB-2001 (first entry)

Human protein tyrosine phosphatase P<sup>Y</sup> LAR cDNA.

KM ppp LAR; protein tyrosine phosphatase; leukocyte antigen related;  
KM human; epithelial cell; cell migration; cell proliferation; cancer;  
KM antitumour; metastasis; antimetastatic; wound healing; vulnery;  
KM diagnosis; gene therapy; ss.

OS Homo sapiens.

FH	Key	Location/Qualifiers
FM		

2  
1  
2  
5  
0  
3  
4  
1  
2  
0

mat nentide

XX 17

XX

XX  
XX

XX  
PB 00-2 PB-1000XX  
PA (PTAC) MAY

PI Ulrich A,

DR WPI; 2000-64

XX  
3

PT migration co  
composition

disclosure:

CC The present

CC negative req

The present sequence is that of cDNA encoding human protein-tyrosine phosphatase PTP LAR (leukocyte antigen related), a negative regulator of epithelial cell migration and tumour

Query Match	99.98;	Score 3463;	DB 21;	Length 7702;
Best Local Similarity	100.08;	Pred. No. 0;		
Matches 3463;	Conservative	0;	Mismatches	0;

[illegible]

QY	785	gattgtgtccatgtttgttgagcggatctgaagacccagaaagagctgtgaaattatagcccaagt	844
Db	5020	gattgtgtccatgtttgttgagcggatctgaagacccagaaagagctgtgaaattatagcccaagt	
QY	845	gaaccctgaagcatcacagaaagaaattacatctgtgtcagaaacggagaaagacaaatagtttcat	5079
Db	5080	gaaccctgaagcatcacagaaagaaattacatctgtgtcagaaacggagaaagacaaatagtttcat	904
QY	905	ccaatgaagcgtctgtcgtgaagagctgtccaaactgttcggccacacaaagaggtgtcgtcccgcaacct	5139
Db	5140	ccaatgaagcgtctgtcgtgaagagctgtccaaactgttcggccacacaaagaggtgtcgtcccgcaacct	964
QY	965	gtatgtcccaacatctccaaagagctgttgagccaaagtgtccccaagggagaaatgtgtaccgcataatga	5199
Db	5200	gtatgtcccaacatctccaaagagctgttgagccaaagtgtccccaagggagaaatgtgtaccgcataatga	1024
QY	1025	gtctcgaattcaaatgttctgttcgcacagatcccaaggcccaacagttcccgcttcatacagcgcaaa	5259
Db	5260	gtctcgaattcaaatgttctgttcgcacagatcccaaggcccaacagttcccgcttcatacagcgcaaa	1084
QY	1085	ccgtgcctctgaacaagaattcaagaagccggtctgtgtgaacatactgtccctatcagatgtgaacgg	5319
Db	5320	ccgtgcctctgaacaagaattcaagaagccggtctgtgtgaacatactgtccctatcagatgtgaacgg	1144
QY	1145	ttgtgtctctgaagcccaatccgtgtgtgttgagaggtctctgtgatactatactgaatgcagattcct	5379
Db	5380	ttgtgtctctgaagcccaatccgtgtgtgttgagaggtctctgtgatactatactgaatgcagattcct	1204
QY	1205	ggaattgtttatgaacagcagaagagccatacagatagtcacaagaggagcctctgtccaaagagagcc	5439
Db	5440	ggaattgtttatgaacagcagaagagccatacagatagtcacaagaggagcctctgtccaaagagagcc	1264
QY	1265	cgagagactctctgcgcacatgtcacaatctggagagcacaattccacacataatgtcatgtgaccaa	5499
Db	5500	cgagagactctctgcgcacatgtcacaatctggagagcacaattccacacataatgtcatgtgaccaa	1324
QY	1325	gcttcggagagatctggcagagagaaatctgccacagatactgtgcacagagagcgtctgtgtccg	5559
Db	5560	gcttcggagagatctggcagagagaaatctgccacagatactgtgcacagagagcgtctgtgtccg	1384
QY	1385	ctaccagttacttctgttcgaacccgaatggtctgagttacaaatctgtccccaatatactctgtcg	5619
Db	5620	ctaccagttacttctgttcgaacccgaatggtctgagttacaaatctgtccccaatatactctgtcg	1444
QY	1445	tgaaattcaaaagttcacagaaatgtcccgagatgtggcagatccaaagaaatcccgacagttcccaagt	5679
Db	5680	tgaaattcaaaagttcacagaaatgtcccgagatgtggcagatccaaagaaatcccgacagttcccaagt	1504
QY	1505	cacagagactgtgcagagacagagtcgtccccaagcagaagagatccatctcggtctccaaagt	5739
Db	5740	cacagagactgtgcagagacagagtcgtccccaagcagaagagatccatctcggtctccaaagt	1564
QY	1565	gcaaggtgtccataaagaccaaagagagcagttgtgaacagagatgtgagccatactcaggtgtcaacgcaag	5799
Db	5800	gcaaggtgtccataaagaccaaagagagcagttgtgaacagagatgtgagccatactcaggtgtcaacgcaag	1624
QY	1625	tgctgtgcgtgtggccgcagaccgggtgtttatactactctgaagcatcgtccctgtgagcgcaatgg	5859
Db	5860	tgctgtgcgtgtggccgcagaccgggtgtttatactactctgaagcatcgtccctgtgagcgcaatgg	1684
QY	1685	ctatgtgagggcgtgtgtgcagatgtttccagaccgtgtgaagaaacctctgtctcaacaaagcgtccgc	5919
Db	5920	ctatgtgagggcgtgtgtgtcagatgtttccagaccgtgtgaagaaacctctgtctcaacaaagcgtccgc	1744
QY	1745	catgtgtgcagacagagagaccagttctacgtgtgtctacgtctgtgcgcctgtgagtaactctgg	5979
Db	5980	catgtgtgcagacagagagaccagttctacgtgtgtctacgtctgtgcgcctgtgagtaactctgg	1804
QY	1805	caggtcttaacacatactcaacgttaactacacgtccctctcctccgcaaccccgccgtg	6039
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QY	1865	gggtcctcgagggagaccagatcctctctgtggccataacggaacatcgttccagcctctctacg	6099
			1924

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Db 6100 gggctcggaggagaccagctctctctgagccatccagacacgctccagccctctcagc 6159
Oy 1925 cagatgctgctactcgcagagacagaccacgggagatccacaggtttcaggagacgttgc 1984
Db 6160 cagatgctgctactcgcagagacagaccacgggagatccacaggtttcaggagacgttgc 6219
Oy 1985 acacaaatcagagagacctaataacatccctgggagagtgagccacagacagacact 2044
Db 6220 acacaaatcagagagacctaataacatccctgggagagtgagccacagacagacact 6279
Oy 2045 gttggcccttctgctacacagacacacacgtgagccgctcctcaagcctctgttgcctcc 2104
Db 6280 gttggcccttctgctacacagacacacacgtgagccgctcctcaagcctctgttgcctcc 6339
Oy 2105 gcatctcagctctctctcctcctggtggggtggtgggcaagcctcctttatacat 2164
Db 6340 gcatctcagctctctctcctcctggtggggtggtgggcaagcctcctttatacat 6399
Oy 2165 taagtgaggtagacagagagatlttagcctctcctcctgatttctccttcggaatcc 2224
Db 6400 taagtgaggtagacagagagatlttagcctctcctcctgatttctccttcggaatcc 6459
Oy 2225 gtaatcgcagagatgggacacgtgtaggggttggtgttaattgtttgttttttttt 2284
Db 6460 gtaatcgcagagatgggacacgtgtaggggttggtgttaattgtttgttttttttt 6519
Oy 2285 ttctgtatgacttctgctgagagacagaaacatgctcctcctcctgagacatggggtgc 2344
Db 6520 ttctgtatgacttctgctgagagacagaaacatgctcctcctcctgagacatggggtgc 6579
Oy 2345 cagcctgagcggaggagctcgccggtggcgaggagacagtgatcagctcctcctcctca 2404
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Oy 2465 ttgtttcctccttaaaagccttttttaagcccaattgacagtgtgagcgaggagaaagt 2524
Db 6700 ttgtttcctccttaaaagccttttttaagcccaattgacagtgtgagcgaggagaaagt 6759
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Db 6880 ctataacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaa 6939
Oy 2705 aaaaaaaagagagcagccttggtctgctcctcaaacctcagaagggagagacact 2764
Db 6940 aaaaaaaagagagcagccttggtctgctcctcaaacctcagaagggagagacact 6999
Oy 2765 cgtgtgctgaggtgctccgagagagcgtgctgctgacgtggccacagagcctgtt 2824
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Db 7060 gttcccgagcctgcaatgagtggtgtgttctgtaggtggtggtgctgtgtggtgc 7119
Oy 2885 aagtgtaataagacaggttagaggtgtgtgacacacacacacacacacacacacacac 2944
Db 7120 aagtgtaataagacaggttagaggtgtgtgacacacacacacacacacacacacacac 7179
Oy 2945 ggcgtgctgctgcttcaagtcagagccagtggtgctgtgtagacatgcttctcctaga 3004

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Db 7180 ggcgtgctgctgcttcaagtcagagccagtggtgctgttagacatgctgtcctcaga 7239
Oy 3005 gcaaggagccagatatttctcctcctggttgcagctgtttcacaagccccagataatcg 3064
Db 7240 gcaaggagccagatatttctcctcctggttgcagctgtttcacaagccccagataatcg 7299
Oy 3065 ctctttcaccctccaaatgacccctcaaaacaaatgtgacagactactgactatc 3124
Db 7300 ctctttcaccctccaaatgacccctcaaaacaaatgtgacagactactgactatc 7359
Oy 3125 aatgtaactcctaagcttcttattatccacagctgtcagagggcagagagcgctct 3184
Db 7360 aatgtaactcctaagcttcttattatccacagctgtcagagggcagagagcgctct 7419
Oy 3185 tcccttgagcagcgctatcagatagtgagtgagtgaggggagggagggatgagctgt 3244
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Oy 3365 gtaaggtcactgtgtgtacacagctgttctcattgttaagaaacacacacacacac 3424
Db 7600 gtaaggtcactgtgtgtacacagctgttctcattgttaagaaacacacacacacac 7659
Oy 3425 tgcataactctgtatgtaataatgttaataatgatttct 3467
Db 7660 tgcataactctgtatgtaataatgttaataatgatttct 7702

RESULT 4
AAZ91908
ID AAZ91908 standard; DNA; 7702 BP.
XX
AC AAZ91908;
XX
DT 07-JUN-2000 (first entry)
XX
DE Human protein tyrosine phosphatase, LAR, coding sequence.
XX
KW Human; protein tyrosine phosphatase; antibody; intracellular domain; LAR;
KW CD45; PTP; diagnosis; insulin resistance related disease; syndrome X;
KW non-insulin dependent diabetes mellitus; arteriosclerosis; therapy;
KW heart disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200002922-A1.
XX
PD 20-JAN-2000.
XX
PF 06-JUL-1999; 99WO-JP03656.
XX
PR 10-JUL-1998; 98WO-JP03120.
XX
PA (FUSO ) FUSO PHARM IND LTD.
XX
PI Yamamoto H, Tsujikawa K, Uchino Y;
XX
DR WPI; 2000-182215/16.
XX
DR P-PSDB; AA81785.
XX
PT Antibody for diagnosis and treatment of insulin resistance disorders
XX and syndrome X recognises the intracellular domains of tyrosine
XX phosphatase
XX
PS Example 1; Page 61-77; 83pp; Japanese.
XX

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50 Sequence 7702 BP; 1636 A; 2286 C; 2292 G; 1488 T; 0 other;

mispatches

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Db	5140	ccatagaggcgcgtgctggaagggctgccaagtctggccacacagaaggtgctgcggccgaacct	5199
QY	965	gtaatgccacatccacagaagcttggtgcccgaagctgctccagaagggaatgtgacccgcatgga	1024
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QY	1025	gctcgaagttcaaaagtctgtgcccagctcccaaggccacagctccctccagcttcacacagcgccaa	1084
Db	5260	gctcgaagttcaaaagtctgtgcccagctcccaaggccacagctccctccagcttcacacagcgccaa	5319
QY	1085	ccctgcctctgcaacaaagttccaaagaaccgggtctgttgaaatctatgcccataagattgaccg	1144
Db	5320	ccctgcctctgcaacaaagttccaaagaaccgggtctgttgaaatctatgcccataagattgaccg	5379
QY	1145	tgtgtgtctgcacaaacccatccgtggtgtggaagggctctgacatacactatgcccagcttccct	1204
Db	5380	tgtgtgtctgcacaaacccatccgtggtgtggaagggctctgacatacactatgcccagcttccct	5439
QY	1205	ggatgtgtataagacacagaaagagccctacatagtctacacaaagggccctctgacagaagacac	1264
Db	5440	ggatgtgtataagacacagaaagagccctacatagtctacacaaagggccctctgacagaagacac	5499
QY	1265	cgagagactctctggcgcacatgctcatggaagacaattccacacacatcatcgtatctgacgaa	1324
Db	5500	cgagagactctctggcgcacatgctcatggaagacaattccacacacatcatcgtatctgacgaa	5559
QY	1325	gcttcctgggaagatggtgacagggaggaatgctccacacagctactgtgcccagagagcgtctgtccg	1384
Db	5560	gcttcctgggaagatggtgacagggaggaatgctccacacagctactgtgcccagagagagcgtctgtccg	5619
QY	1385	ctaccagactatttgtgtgacccgaatggtcgtgaattacaacatgcccacagctatatctccgg	1444
Db	5620	ctaccagactatttgtgtgacccgaatggtcgtgaattacaacatgcccacagctatatctccgg	5679
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Db	5740	cacagactctggccagagacagggcgtgcccacaaagacggaggaattcatctgacttccatccgg	5799
QY	1565	gcaggtgtcatataagaccaaagagacatttgggacagaatggtgacctatccaggtgtgacctgacg	1624
Db	5800	gcaggtgtcatataagaccaaagagacatttgggacagaatggtgacctatccaggtgtgacctgacg	5859
QY	1625	tgtctggcgttggggccggacacgggggtgttcatcatccttgtagatcatcgtcccttggaaggatggtg	1684
Db	5860	tgtctggcgttggggccggacacgggggtgttcatcatccttgtagatcatcgtcccttggaaggatggtg	5919
QY	1685	ctataagagggcgtgtgctgcgaacatgcttccaagaaccgttggaaagaccctctgataacacagctctgc	1744
Db	5920	ctataagagggcgtgtgctgcgaacatgcttccaagaaccgttggaaagaccctctgataacacagctctgc	5979
QY	1745	catgtgtgcagaagaaggggcccagctatcagctgtgtctacccgttgccgcccctggagtaacctgg	1804
Db	5980	catgtgtgcagaagaaggggcccagctatcagctgtgtctacccgttgccgcccctggagtaacctgg	6039
QY	1805	cagctttgacacatgctacaagcttaactacacagcgtccctctctccgacacaccccgcgctg	1864
Db	6040	cagctttgacacacatgctacaagcttaactacacagcgtccctctctccgacacaccccgcgctg	6099
QY	1865	gggtctccggaaagggaacccagctctctctgacacataccgacatcgtctccagcctctctacg	6159
Db	6100	gggtctccggaaagggaacccagctctctctgacacataccgacatcgtctccagcctctctacg	1924
QY	1925	caagatctgtactctgccaagacacacacacacgggggaatcaacagcttccaggaacgtttgcc	1984
Db	6160	caagatctgtactctgccaagacacacacacacgggggaatcaacagcttccaggaacgtttgcc	6219

**RESULT 5**

AA59133  
ID AA59133 standard; DNA: 7702 BP.

AC AA59133;  
XX XX  
XX XX  
DT 17-APR-2000 (first entry)  
DE LAR tyrosine phosphatase complete gene.  
KW Intracellular domain; P-subunit; human; leucocyte antigen related; LAR  
KW tyrosine phosphatase; antibody; thyroid cancer; ds.  
OS Homo sapiens.  
PN WC964591-A1.  
PD 16-DEC-1999.  
PE 07-JUN-1999; 99WO-JP03054.  
PR 08-JUN-1998; 98WO-JP02542.  
PS (FUSO ) FUSO PHARM IND LTD.  
PI Yamamoto H, Tsujikawa K, Uchino Y, Konishi N;  
DR WPI: 2000-097538/08.  
XX P-PSDB: AAY56100.  
XX  
PT Antibody recognizing the intracellular domain of the human tyrosine  
XX phosphatase LAR .  
PS Disclosure; Page 81-97; 104pp; Japanese.  
XX  
CC This sequence represents the complete coding region for the human  
CC leucocyte antigen related (LAR) tyrosine phosphatase. The invention  
CC domain of the generation of an antibody recognizing the intracellular  
CC used for the diagnosis and treatment of thyroid cancer. The antibody "is  
XX  
XX Sequence 7702 BP; 1636 A; 2286 C; 2292 G; 1488 T; 0 other;

[illegible]

Db 6340 gaattctcatgctctctctcataggggttggtgggcaagcctcctttaaatacat 6399  
Oy 2165 taagtgggtagaacttgagggaatttagcctctccctctgaatttctcttcgcaatcc 2224  
Db 6400 taagtgggtagaacttgagggaatttagcctctccctctgaatttctcttcgcaatcc 2224  
Oy 2225 gtaatcgaagaatgggcaacttgagggttggtggtattatctgtttttttttt 2284  
Db 6460 gtaatcgaagaatgggcaacttgagggttggtggtattatctgtttttttttt 2284  
Oy 2285 ttgttatgactctctctgaagaagacaaatctgctctctctctgaagcggggctgc 2344  
Db 6520 ttgttatgactctctctgaagaagacaaatctgctctctctctgaagcggggctgc 2344  
Oy 2345 cagcccgagcgagggctctgcccgttgccggggaagcagtgctgatacgcgcctccca 2404  
Db 6580 cagcccgagcgagggctctgcccgttgccggggaagcagtgctgatacgcgcctccca 2404  
Oy 2405 gccctcagaagagatccctgttctcagcaaatgcaaggaaactaaatgtttttaagt 2464  
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Db 6880 ttaaaaaaacaacaaacacacaaataaaaaaacaacaaacaaacaaacaaacaa 2704  
Oy 2705 aaaaaaagaagtagcctctgctctgcttcaaacctcagaagaggagaactc 2764  
Db 6940 aaaaaaagaagtagcctctgctctgcttcaaacctcagaagaggagaactc 2764  
Oy 2765 cgtgtccttgagggttcccgaggagcgtgctgctgaacctgggcccacagagcctgctt 2824  
Db 7000 cgtgtccttgagggttcccgaggagcgtgctgctgaacctgggcccacagagcctgctt 2824  
Oy 2825 ggtcccaagcattgacagtagtggtgtgtgttagagcgtggtgggtcgtgtgtgccc 2884  
Db 7060 ggtcccaagcattgacagtagtggtgtgtgttagagcgtggtgggtcgtgtgtgccc 2884  
Oy 2885 aaggtgaatagacaggttaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2944  
Db 7120 aaggtgaatagacaggttaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2944  
Oy 2945 ggcgtggtgcttccatcagtcagcagcagtcagtcagtcagtcagtcagtcagtcagtc 3004  
Db 7180 ggcgtggtgcttccatcagtcagcagcagtcagtcagtcagtcagtcagtcagtcagtc 3004  
Oy 3005 gcaaggagcagatgatttctcctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3064  
Db 7240 gcaaggagcagatgatttctcctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3064  
Oy 3065 cctcttccctcacaagatgctcctcacaagatgctcctcacaagatgctcctcacaagatg 3124  
Db 7300 cctcttccctcacaagatgctcctcacaagatgctcctcacaagatgctcctcacaagatg 3124  
Oy 3125 aatgttaacttaactcagtccttatacccaagtcgtgaggggagagagagagagagagag 3184  
Db 7360 aatgttaacttaactcagtccttatacccaagtcgtgaggggagagagagagagagagag 3184  
Oy 3185 tccctcgggagcagctatctatagtaagtgggggaggggagggagagagagagagagagag 3244  
Db 7420 tccctcgggagcagctatctatagtaagtgggggaggggagggagagagagagagagagag 3244

Oy 3345 taagtgggagcgttggtgcccagctccccaacactagctaggctaaagtaaatcaatc 3304  
Db 7480 taagtgggagcgttggtgcccagctccccaacactagctaggctaaagtaaatcaatc 3304  
Oy 3305 tccagggttgtaagtgtgataatgaacattcttcttactctgtgagtagtgct 3364  
Db 7540 tccagggttgtaagtgtgataatgaacattcttcttactctgtgagtagtgct 3364  
Oy 3365 gtagagttacgt 3424  
Db 7600 gtagagttacgt 3424  
Oy 3425 tgcataatcttgatgtaataaattgataatcaagttctc 3467  
Db 7660 tgcataatcttgatgtaataaattgataatcaagttctc 3467  
RESULT 6  
ID AAF15575 standard; cDNA: 3064 BP.  
AC AAF15575;  
XX 13-MAR-2001 (first entry)  
DT 13-MAR-2001 (first entry)  
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:10.  
KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;  
KW neuroprotective; cytosolic; cardioactive; immunomodulatory; muscular;  
KW vulnary; gastrointestinal; nephrotoxic; anti-infective; gynaecological;  
KW antibacterial; gene therapy; neural; immune; reproductive; renal;  
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
KW wound; infectious disease; ss.  
OS Homo sapiens.  
XX  
XX WO200055174-A1.  
PN 21-SEP-2000.  
PD 08-MAR-2000; 2000WO-US05988.  
PF 12-MAR-1999; 99US-0124270.  
PR (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
XX  
XX Rosen CA, Ruben SM.  
PI WPI: 2000-587513/55.  
DR P-PSDB: AAB56372.  
XX  
XX Prostate cancer associated gene sequences, referred to as prostate  
XX cancer antigens, useful for treatment, prevention, and diagnosis of  
XX disorders such as prostate cancer.  
PS Claim 1: Page 621-622; 2338bp; English.  
XX  
XX AAF15566 to AAF16505 encode the human prostate cancer associated  
XX proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.  
XX The prostate cancer antigens can have neuroprotective, cytosolic,  
XX cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,  
XX nephrotoxic, anti-infective, gynaecological and antibacterial activities,  
XX and can be used in gene therapy. The prostate cancer antigen  
XX polynucleotides may be used for detection of prostate cancer, chromosome  
XX identification, as chromosome markers, and for numerous other diagnostic  
XX or research purposes. The prostate cancer antigens may be used to treat  
XX disorders such as neural, immune, muscular, reproductive,  
XX gastrointestinal, pulmonary, cardiovascular, renal, and proliferative.  
XX disorders, wounds, and infectious diseases. AAF15566 to AAF16514 to  
XX AAB57303 represent sequences used in the exemplification of the present  
XX invention.



XX Sequence 3064 BP; 695 A; 820 C; 845 G; 700 T; 4 other:  
SQ

Query Match: 84.1%; Score 2914.4; DB 21; Length 3064;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 2960; Conservative 1; Mismatches 3; Indels 25; Gaps 2;

OY 501 gccctgtgacacgagaccgtgtgacctatctacggtgacacctgtgtgaaacagtgagactg 560  
DB 1 gccctgtgacacgagaccgtgtgacctatctacggtgacacctgtgtgaaacagtgagactg 560  
OY 561 gccacatcacctgtgacacctctgcaactccacaaagatgggtccacagtgaaagcgtgag 620  
DB 61 gccacatcacctgtgacacctctgcaactccacaaagatgggtccacagtgaaagcgtgag 620  
OY 621 ctgtgctacagttcagttcagttcagttcagttcagttcagttcagttcagttcagttcag 680  
DB 121 ctgtgctacagttcagttcagttcagttcagttcagttcagttcagttcagttcagttcag 680  
OY 681 atccctgacctctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 180  
DB 181 atccctgacctctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 180  
OY 741 gtgcaactgacagcgtggtgtggtggtggtggtggtggtggtggtggtggtggtggtggt 800  
DB 241 gtgcaactgacagcgtggtgtggtggtggtggtggtggtggtggtggtggtggtggtggt 800  
OY 801 gagcgtgataagacagagaaagacgtgtgacatctatgtgacacgtgtgacacgtgtgac 860  
DB 301 gagcgtgataagacagagaaagacgtgtgacatctatgtgacacgtgtgacacgtgtgac 860  
OY 861 cagaggaactacatgtgtgacagagagagagagagagagagagagagagagagagagag 920  
DB 361 cagaggaactacatgtgtgacagagagagagagagagagagagagagagagagagagag 920  
OY 921 gagcgtgacacgtgtgacacagagagagagagagagagagagagagagagagagagag 980  
DB 421 gagcgtgacacgtgtgacacagagagagagagagagagagagagagagagagagagag 980  
OY 981 aagctgtgacacgtgtgacacagagagagagagagagagagagagagagagagagagag 480  
DB 481 aagctgtgacacgtgtgacacagagagagagagagagagagagagagagagagagagag 480  
OY 1041 ctgtgacacgtgtgacacag 540  
DB 541 ctgtgacacgtgtgacacag 540  
OY 1101 ttcaagaacacgtgtgacacagagagagagagagagagagagagagagagagagagag 600  
DB 601 ttcaagaacacgtgtgacacagagagagagagagagagagagagagagagagagagag 600  
OY 1161 atccgt 1220  
DB 661 atccgt 1220  
OY 1221 cagagagacctacatgacacagagagagagagagagagagagagagagagagagagag 1280  
DB 721 cagagagacctacatgacacagagagagagagagagagagagagagagagagagagag 1280  
OY 1281 atgtcattgt 1340  
DB 781 atgtcattgt 1340  
OY 1341 agggagaaatgtgacacag 1400  
DB 841 agggagaaatgtgacacag 1400  
OY 1401 gtgtgacacgt 1460  
DB 901 gtgtgacacgt 1460  
OY 1461 gatgcccggatgt 1520

DB 961 gatgcccggatgt 1020  
OY 1521 cagagagacctacatgacacag 1580  
DB 1021 cagagagacctacatgacacagagagagagagagagagagagagagagagagagagag 1580  
OY 1581 aaggaacagttgt 1640  
DB 1081 aaggaacagttgt 1640  
OY 1641 accggt 1700  
DB 1141 accggt 1700  
OY 1701 gacatgt 1760  
DB 1201 gacatgt 1760  
OY 1761 gacacgt 1820  
DB 1261 gacacgt 1820  
OY 1821 gcaacgt 1880  
DB 1321 gcaacgt 1880  
OY 1881 ccagctgt 1940  
DB 1381 ccagctgt 1940  
OY 1941 cagagacacagcag 2000  
DB 1441 cagagacacagcag 2000  
OY 2001 ctgaagaacacgt 1500  
DB 1501 ctgaagaacacgt 1500  
OY 2061 ccagacacacgt 2120  
DB 1561 ccagacacacgt 2120  
OY 2121 ttctcattgt 1620  
DB 1621 ttctcattgt 1620  
OY 2181 agggattttagcctctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 2240  
DB 1681 agggattttagcctctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 2240  
OY 2241 ccactgt 2281  
DB 1741 ccactgt 2281  
OY 2282 -----tt 1800  
DB 1801 tccattatt 1800  
OY 2339 ggcctgacagcctgt 1920  
DB 1861 ggcctgacagcctgt 1920  
OY 2399 cctccagacccctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 2458  
DB 1921 cctccagacccctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 2458  
OY 2459 taagt 1980  
DB 1981 taagt 1980  
OY 2519 gaagataaggaaac 2578





Accession	Sequence	Position
Oy	gttccatcaatctcgtgcatcgtctctgtgagcgatgcgtatcgtagagcgctgttcgacatgtt	1706
Dh		
Dh	cttccatcaatcgtcttaacatcgtctgtcgagcgatgcgtatcgtagagcgctgttcgacatctt	5637
Oy	tgaagacggtgaagacccctcgtcttaacagcgctctctgcattgtgcagacagagaccatga	1766
Dh		
Dh	tcagacggttgaaagatgcatcaagaaacccagcgccgcatatgtgcagacagagatgagta	5697
Oy	tcagctctgtcatcgtctgcgcgcgtgatactccgcgcacatttgacacatatgcagcga	1828
Dh		
Dh	ccagctctgttatccagcgcgcgcgtacgtctccctcgcgaagacttgcaccatatgcacatta	5757
Oy	actacgcgtcccccctctctctccgcacccc	1857
Dh		
Dh	aagccatggtctcccccagcgcgcgcagaca	5786

RESULT	8	
AAAT85389		
ID	AAAT85389	standard; cDNA; 6000 BP.
XX		
AC	AAAT85389;	
XX		
DT	19-DEC-1997	(first entry)
XX		
DE	Human protein tyrosine phosphatase PTP-OB encoding cDNA.	
XX		
KM	Protein tyrosine phosphatase' PTP-OB; PTPepasiloni; osteoblast;	
KM	recombinant protein; growth; differentiation; brain; human; ss.	
OS		
XX	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	CDS	23..5758
FT		/*tag=
XX		/product= PTP-OB
PN		
XX	US5658756-A.	
PD		
XX	19-AUG-1997.	
PF	14-SEP-1993;	93US-0122032.
XX		
PR	01-DEC-1994;	94US-0348006.
PR	14-SEP-1993;	93US-0122032.
XX		
PA	(MERI ) MERCK & CO INC.	
PI		
XX	Rodan GA, Rutledge SJ, Schmidt A;	
DR	WPI; 1997-424232/39.	
DR	P-PSDB; AAM27225.	
XX		
PT	DNA encoding protein tyrosine phosphatase PTP-OB - Isolated from	
PT	human osteoblasts and useful for production of recombinant PTP-OB	
XX		
PS	Claim 2; Column 33-38; 34pp: English.	
XX		
CC	The present sequence represents an isolated and purified DNA molecule	
CC	encoding human protein tyrosine phosphatase (PTP-OB) protein. The DNA	
CC	is useful for production of the recombinant protein, which is a	
CC	protein tyrosine phosphatase which may be involved in the growth and	
CC	differentiation of osteoblasts and brain cells and is useful for	
CC	identifying compounds that modulate PTP-OB activity and as a therapeutic	
XX	for treating PTP-OB-related diseases.	

Query Match 37.1% Score 1285; DB 18; Length 6000;  
Best Local Similarity 81.4%  
Pred. No. 2,1e-27;  
Matches 1489; Conservative 0; Mismatches 340; Indels 0; Gaps 0

```

OY 29 ccactctctgacccctgtgagatgcggaggtcctaactacagaccacggatgtcgaga 88
Db 3958 ccacccaaagagaccctgtgtgaaatgagacgcatiaacttcagactccagatcgatcttag 4017
OY 89 ccaacccacccatcccatcaaccacgttgcgcagacacatcagagcgtctcaaaagcaacga 148
Db 4018 ccaacccgacatcccatcgtcagacatggtgcgagccacagagcggtccaaagcgcaacaga 4077
OY 149 tggcttcaagttctccagagatagatcctacacccttgagacagagcttcaagttgaga 208
Db 4078 cagcttcaagctctcccaagagatagatcctacacccttgagacagagcttcaagttgaga 4137
OY 209 gaattcaaacctggaggtgaaacagcccaagaaccgcatctcgaaatgtcatcgcttaga 268
Db 4138 acattccaaaccctggaggtgaaacagcccaagaaccgcatctcgaaatgtcatcgcttaga 4197
OY 269 ccaactctgagtcataccttataccttataccttataccttataccttataccttatacct 328
Db 4198 ccaactctgagtcataccttataccttataccttataccttataccttataccttatacct 4257
OY 329 caactacatcgaatgctcagcgcagacaggaatgctacatcgcagcagagcccgctgc 388
Db 4258 caactacatcgaatgctcagcgcagacaggaatgctacatcgcagcagagcccgctgc 4317
OY 389 cgaagacatggtgcgaattctctgagaaatgtgtgtggaacagcgcagcgcagcgtgtcat 448
Db 4318 tgaagccttctgagacatctctgagaaatgtgtgtggaacagcgcagcgcagcgtgtcat 4377
OY 449 gatgaacaggtctgagagaggaagtcgcgggtcaaaatgtgatcaatctgtgcaacccgtg 508
Db 4378 gatgaacaggtctgagagaggaagtcgcgggtcaaaatgtgatcaatctgtgcaacccgtg 4437
OY 509 caacgagacctgtgtgcttataccttgcaggtgcagcgtgtggaacaggtgtgagcttgcacata 568
Db 4438 caacgagacctgtgtgcttataccttgcaggtgcagcgtgtggaacaggtgtgagcttgcacata 4497
OY 569 cactgtgcgacacttgcacatccacagagatgtgtcctcagatgagataccatcgtgcacata 628
Db 4498 ctgtgtcagagacatctctctgcacagagatgtgtcctcagatgagataccatcgtgcacata 4557
OY 629 gtctcagatgagcgtgtgcgcagacacatgagatgtctgtgagacaggtgtgagcttgcacata 688
Db 4558 gtctcagatgagcgtgtgcgcagacacatgagatgtctgtgagacaggtgtgagcttgcacata 4617
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Db 4618 ctctcctacagcgtgtcagagctgtgcaacccctagacagcagagccatgtgtgtgacgtg 4677
OY 749 cagcgtgcgtgtgtgcgcagcgcgtgtgtcctcagatgagcagagccatgtgtgtgacgtg 808
Db 4678 cagcgtgcgtgtgtgtgcgcagcgcgtgtgtcctcagatgagcagagccatgtgtgtgacgtg 4737
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Db 4738 caagcagagagagagcgtgtgacatctatgtgcacagctgtgcagcagcagagagagaa 4797
OY 869 ctacatgtgtgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 928
Db 4798 ctacatgtgtgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 987
OY 929 cactgtgcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 988
Db 4858 gggcgtgtgtgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 4917
OY 989 ccaatgtgtgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1048
Db 4918 ccaatgtgtgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 4977
OY 1049 ctcaagagccacagcgtctcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1108
Db 4978 ctcaagagccacagcgtctcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5037

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OY 1109 ccggtgtgtgacatcagcgtcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1168
Db 5038 ccggtgtgtgacatcagcgtcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5097
OY 1169 tgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1228
Db 5098 tgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5157
OY 1229 ctacatgtgtgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1288
Db 5158 ctacatgtgtgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5217
OY 1289 gtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5277
Db 5218 gtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5337
OY 1349 atgcacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1408
Db 5278 atgcacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5337
OY 1409 gatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1468
Db 5338 gatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5397
OY 1469 gtagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1528
Db 5398 gtagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5457
OY 1529 gccacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1588
Db 5458 gccacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5517
OY 1589 gttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1648
Db 5518 gttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5577
OY 1649 gtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1708
Db 5578 gtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5637
OY 1709 tcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1768
Db 5638 tcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5697
OY 1769 tcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1828
Db 5698 tcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5757
OY 1829 actacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1887
Db 5758 actacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5817

RESULT 9
AAK06095
ID AAK06095 standard; cDNA: 6000 BP.
XX
AAK06095;
XX
01-APR-1999 (first entry)
DE
XX
Human protein tyrosine phosphatase (PTP-OB) encoding cDNA.
KW
osteoporosis; cancer; ss.
OS
Homo sapiens.
XX
Key Location/Qualifiers
CDS 23..5758
FT /tag= a
FT /product= "PTP-OB"
XX

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PN US866397-A.  
 XX 02-FEB-1999.  
 PD 14-FEB-1997: 97US-0800825.  
 XX 01-DEC-1994: 94US-0348006.  
 PR 14-SEP-1993: 93US-0122032.  
 PR 14-FEB-1997: 97US-0800825.  
 XX (MERI) MERCK & CO INC.  
 PI Rodan GA, Rutledge SJ, Schmidt A;  
 XX WPI: 1999-141930/12.  
 DR P-PSDB: AAW94027.  
 XX  
 PT Protein tyrosine phosphatase denoted PTP-OB - useful for drug  
 screening  
 PS Examples: Columns 33-38: 34pp: English.  
 CC This cDNA encodes a human protein tyrosine phosphatase (PTP) denoted as  
 CC PTP-OB, produced by bone and brain cells. A recombinant host cell  
 CC transfected or transformed with a nucleic acid vector comprising the  
 CC nucleic acid can be used for the production of the PTP-OB polypeptide.  
 CC The protein can be used to screen for modulators of PTP-OB activity.  
 CC Which might be useful for treating e.g. osteoporosis and cancer.  
 CC  
 SO Sequence 6000 BP: 1229 A; 1971 C; 1803 G; 997 T; 0 other:

Query Match 37.1%; Score 1285; DB 20; Length 6000;  
 Best Local Similarity 81.4%; Pred. No. 2.1e-271;  
 Matches 1489; Conservative 0; Mismatches 340; Indels 0; Gaps 0:

OY 29 ccaatctctgagccctgtgagatgctggaagctcaactacacagccacagccagatgagaga 88  
 DB 3558 ccaccacaaagaccctgtgaaatgagacgcatctaactccagactccagcagatgcttag 4017  
 OY 89 ccaaccacccacccctcctacccctgctgagcaacacatcagagcgctcacaagacaaaga 148  
 DB 4018 ccaccgcgcaatcccatctgcagacacatgagcagacagagcgctcacaagacaaaga 4077  
 OY 149 tggcctcaagctctccagagagatgagtcacatcagaccctgagacagcgatgagtgga 208  
 DB 4078 cagcctcaagctctccagagagatgagtcacatcagaccctgagacagcgatgagtgga 4137  
 OY 209 gaattcaaacctggaagtgaaacaaagccaaagacgctatcgaaatgcatcgctcaga 268  
 DB 4138 acattcacaacctggaagtgaaacaaagccaaagacgctatcgaaatgcatcgctcaga 4197  
 OY 269 ccaactctgagatcctcactatcagatgagcgctcccgaggatgagctacatcagtc 328  
 DB 4198 ccaactctgagatcctcactatcagatgagcgctcccgaggatgagctacatcagtc 4257  
 OY 329 caactacacagctgagctacccgcaagcagaatgctacatcgccaagagggccctcgc 388  
 DB 4258 caactacacagctgagctacccgcaagcagaatgctacatcgccaagagggccctcgc 4317  
 OY 389 ggaagcacttggagatctctcggagaatgctgagaaacagagcgccacgttggatc 448  
 DB 4318 tgaagcacttggagatctctcggagaatgctgagaaacagagcgccacgttggatc 4377  
 OY 449 gatgacagctgagagagagagctcccggttaaaatgtagacagatcagccagcggtg 508  
 DB 4378 gatgacagctgagagagagagctcccggttaaaatgtagacagatcagccagcggtg 4437  
 OY 509 caccagagacctgtgcttactcagtgagaccgttggacacagtgagagctggccacata 568  
 DB 4438 caccagagacctgtgcttactcagtgagaccgttggacacagtgagagctggccacata 4497  
 OY 569 cactgtgacaccttcgactccacaaagatgctccagtgagaaagcgtgagctgcgtca 628

DB 4498 ctgcgtcagagacatctctctgcacaaagatgctccagtgagaacgaggtccgca 4557  
 OY 629 gtccaagatgagctgctgcagacacatgagatctctgtgataccaactccatctggc 688  
 DB 4558 gtccaagatgagctgctgcagacacatgagatctctgtgataccaactccatctggc 4617  
 OY 689 ctccaagatgagctgctgcagacacatgagatctctgtgataccaactccatctggc 748  
 DB 4618 ctccaagatgagctgctgcagacacatgagatctctgtgataccaactccatctggc 4677  
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PN WO9509656-A.  
 PD 13-APR-1995.  
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 PF 30-SEP-1994; 94WO-US11163.  
 XX  
 PR 01-OCT-1993; 93US-0130570.  
 XX  
 PA (UWNY ) UNIV NEW YORK STATE.  
 XX  
 PI Schlessinger J, Yan H;  
 XX  
 DR WPI; 1995-155068/20.  
 DR P-PSDB; AAR72858.  
 XX  
 PR Novel, isolated receptor-type protein tyrosine phosphatase-sigma  
 XX - and encoding DNM, useful e.g. for detecting neuro-blastomas  
 XX Claim 7; Figure 2; 105pp; English.  
 CC Ligands binding to the receptor-type protein tyrosine phosphatases

810 aaagcaccgaaacacgcgtgaacatctttcaaacatttgcggcgcatc 4318

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Db 4319 agaacagagaaacggtgtagtgcagacacgtgacactcatctcgtctacacagcgaac 4378
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Db 4499 caggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1049
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Db 4739 tacatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1289
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Db 4799 gtagcacaatccacacacacacacacacacacacacacacacacacacacacacacacacac 1349
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RESULT 11
ID AA094311 standard: cDNA to mRNA; 4555 BP.
AC AA094311;
DT 10-MAY-1996 (first entry)
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XX Tyrosine phosphatase MPTP-delta cDNA.
DE
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XX Tyrosine phosphatase MPTP-delta; murine; brain tissue;
KW glutathione-S-transferase; fusion protein; E. coli; differentiation;
KW activation; information transmission; nervous system; immune system;
XX carcinogenesis; ds.
XX
XX Mus musculus domesticus.
OS
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XX Key Location/Qualifiers
FH 5'UTR 1..477
FT /tag= a
FT CDS 478..4353
FT /tag= b
FT /product= MPTP-delta
FT 3'UTR 4354..4555
FT /tag= c
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XX JP07236487-A.
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XX 12-SEP-1995.
XX
XX 28-FEB-1994; 94JP-0054726.
XX
XX 28-FEB-1994; 94JP-0054726.
XX
XX (TOKS-) TOKYO SHINKAI KAGAKU SOGO KENKYUSHO ZH.
XX
XX MPT. 1995-347455/45.
XX
XX P-PSDB: AAR75201.
XX
XX DNA encoding tyrosine phosphatase MPTP delta - useful for
XX elucidation of signal transmission mechanisms.
XX
XX Claim 1: Page 5-11; 14p; Japanese.
XX
XX This sequence represents the tyrosine phosphatase MPTP-delta coding
XX sequence. This sequence was isolated from murine brain tissue and
XX was cloned, for expression, into the downstream region of a
XX glutathione-S-transferase sequence and expressed as a fusion protein
XX in E. coli. MPTP-delta proteins regulate differentiation and
XX activation of cells. This sequence can be used in the elucidation of
XX the molecular mechanism for information transmission in cells,
XX the mechanism of carcinogenesis.
XX
XX Sequence 4555 BP; 1374 A; 986 C; 1032 G; 1163 T; 0 other.
XX
Query Match 30.5%; Score 1059; DB 16; Length 4555;
Best Local Similarity 75.2%; Pred. No. 5,1e-222;
Matches 1362; Conservative 0; Mismatches 440; Indels 9; Gaps 3;
Oy 29 ccacccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2562
Db 2562 ccacccacacacacacacacacacacacacacacacacacacacacacacacacacacacacac 2621
Oy 89 ccacccacacacacacacacacacacacacacacacacacacacacacacacacacacacacac 148
Db 2622 ccacccacacacacacacacacacacacacacacacacacacacacacacacacacacacacac 2681
Oy 149 tggcctcaagttctccagagatgatgtcatcgaacccctgtgacagacgttcacgtgtgtgtgtgt 208

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Db 2682 taacctgaagtttcccggaatatgtcaattgacctgcccagtcagttacatgagg 2741  
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 Db 2742 aactcaaaacttggaagttgacaagaagcccaagaacccgtatgcaagatgctgctacga 268  
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 AC AAX24802;  
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 DT 21-JUN-1999 (first entry)  
 DE Leukocyte antigen related protein tyrosine phosphatase domain DNA.  
 XX Leukocyte antigen related protein tyrosine phosphatase; LAR41;  
 KW human; T7 promoter; operator; gene expression; vector; pZRV3.3;  
 KM de.  
 OS Homo sapiens.  
 OS Homo sapiens.  
 PN MO905297-A1.  
 PN MO905297-A1.  
 PD 04-FEB-1999.  
 PD 04-FEB-1999.  
 PF 21-JUL-1998; 98MO-G802175.  
 PF 21-JUL-1998; 98MO-G802175.  
 PR 25-JUL-1997; 97GB-0015660.  
 PR 25-JUL-1997; 97GB-0015660.  
 PA (ZENNE) ZENNECA LTD.  
 PA (ZENNE) ZENNECA LTD.  
 PI Bunde11 KR, Hockney RC, Kara BV, Plo11 D;  
 PI Bunde11 KR, Hockney RC, Kara BV, Plo11 D;  
 DR WPI; 1999-142947/12.  
 DR WPI; 1999-142947/12.  
 XX New system for expression of recombinant proteins - comprises a T7





CC sequence tags (SESTs), isolated from human, mouse, chicken and rat  
 CC tissue sources. The SESTs can have a range of activities depending on  
 CC the tissues they were isolated from. The activities include:  
 CC chemotactic; proliferative; immunomodulatory; haematopoietic;  
 CC chemokinetic; analgesic; haemostatic; thrombolytic; anti-inflammatory;  
 CC cytostatic; antibacterial; antifungal; antiviral; antidiabetic;  
 CC antiallergic; antiparasitic; antiproliferative; antineoplastic;  
 CC antitumor; antipain; antipruritic; antipruritic; antipruritic;  
 CC anticonvulsant; antiepileptic; antiepileptic; antiepileptic;  
 CC therapy and in vaccines. The SESTs are useful as probes for gene  
 CC identification and isolation of full-length cDNAs and genomic DNA  
 CC molecules which correspond to the SESTs. Proteins encoded by the SESTs  
 CC are useful in assays for determining biological activity and raising  
 CC antibodies. They may be useful for treatment of autoimmune disorders  
 CC (multiple sclerosis, insulin dependent diabetes), allergic conditions  
 CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,  
 CC osteoporosis, osteoarthritis, central nervous system disorders  
 CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation  
 CC disorders (hemophilia, thrombosis), inflammatory disorders (Crohn's  
 CC disease), tumours, bacterial, fungal or viral infections, depression and  
 CC psoriasis. AAA45926 to AAA45931 represent linker variants which are given  
 CC in the exemplification of the present invention.  
 CC  
 CC Sequence 601 BP; 130 A; 175 C; 189 G; 107 T; 0 other;

Query Match 16.7%; Score 578.4; DB 21; Length 601;  
 Best Local Similarity 99.8%; Pred. No. 2.9e-117;  
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OY 452 gacacgctggagagagagtcctccggttaaatgtatcagctgacacccctggcac 511  
 DB 22 gacacgctggagagagagtcctccggttaaatgtatcagctgacacccctggcac 81  
 OY 512 cgaagcctgtgctctattcagtgagctgttgacacagtgagctgacacacac 571  
 DB 82 cgaagcctgtgctctattcagtgagctgttgacacagtgagctgacacacac 141  
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 DB 142 tgtgacaccttgac 201  
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 DB 202 tcaatcattgctgctgacacacacacacacacacacacacacacacacacacac 261  
 OY 692 cctacgacggtcgaagcctgacacacacacacacacacacacacacacacacacac 751  
 DB 262 cctacgacggtcgaagcctgacacacacacacacacacacacacacacacacacac 321  
 OY 752 cggcggtgtggtgac 811  
 DB 322 cggcggtgtggtgac 381  
 OY 812 gacacgag 871  
 DB 382 gacacgag 441  
 OY 872 catggtgacgag 931  
 DB 442 catggtgacgag 501  
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 DB 502 gtcggtgac 1031  
 OY 992 agtgcctcag 561  
 DB 562 agtgcctcag 601

RESULT 14  
 AAQ21001

ID AAQ21001 standard; DNA; 2872 BP.  
 XX AAQ21001;  
 AC 28-MAY-1992 (first entry)  
 DT 28-MAY-1992 (first entry)  
 DE Murine receptor-type protein tyrosine phosphatase gene.  
 XX R-PTase; cellular metabolism; cancer; diabetes; mouse; 99.  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 259..2640  
 FT /tag= a  
 PN MO9201050-A.  
 PD 23-JAN-1992.  
 PF 11-JUL-1991; 91MO-US04892.  
 PR 26-FEB-1991; 91US-0654188.  
 PR 11-JUL-1990; 90US-0551270.  
 PA (UNIV-) NEW YORK UNIV.  
 XX  
 PI Schlessinger J;  
 DR WP1; 1992-056865/07.  
 DR P-PSDB; AAR20743.  
 XX  
 PT Human receptor-type protein tyrosine phosphatase - has DNA  
 PT encoding. It and antibodies specific for it, useful for screening  
 PT drugs affecting R-PTase activity, and detection of mutant genes  
 XX  
 PS Claim 7; Fig 1; 77pp; English.  
 XX  
 CC The sequence is that of the gene encoding mouse receptor-type  
 CC protein tyrosine phosphatase (R-PTase). It may be used to produce  
 CC the R-PTase recombinantly. Probes may be designed from the gene  
 CC that can be used to detect mutant genes in PCR amplification and  
 CC hybridisation assays.  
 CC  
 CC Sequence 2872 BP; 785 A; 721 C; 724 G; 642 T; 0 other;

Query Match 15.9%; Score 552; DB 13; Length 2872;  
 Best Local Similarity 59.5%; Pred. No. 3.3e-111;  
 Matches 977; Conservative 0; Mismatches 650; Indels 15; Gaps 2;

OY 195 cagttcagctggag 254  
 DB 991 cagttcagctggag 1050  
 OY 255 gtcacgtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 314  
 DB 1051 atctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 374  
 OY 315 gactacatcaatgac 434  
 DB 1111 gactacatcaatgac 494  
 OY 435 gacacgtggtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 554  
 DB 1231 gacacgtggtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1290  
 OY 495 tggcagcccggtgac 1354

[illegible]

AA736881

AA  
AC  
AA736XX  
DE

DE  
Murina

**KW** **Murline**

cellulose

diabet

XX

CDS

US55381

**X**

10-FEB-

26-FEB-

(intro)

100

1. odd,

potenti:

The pres

CC phosphatase sequence encodes murine receptor type tyrosine  
CC CDNA library screened with a probe encoding the intracellular and  
CC transmembrane domains of human 7200 glycoprotein. RPTP are  
CC potential anti-oncogenes and effectors in transmembrane signaling  
CC They can be used to screen for cpds. which are specific activators  
CC or inhibitors, for modulating cellular metabolism. Cpds that  
CC activate RPTP cause dephosphorylation and so might prevent cell  
CC growth and oncogenic transformation, while over activity of RPTP  
CC may be involved in diabetes susceptibility. Detection of normal or

123 A; 123 C; 124 G; 642 T; 0 other;

QY	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300
QY	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300

[illegible]

Search completed: August 21, 2001, 20:30:20  
Job time: 7623 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2001, 18:17:52 ; Search time 2512.41 Seconds  
(without alignments)

13044.465 Million cell updates/sec

Title: US-09-719-272-1  
Perfect score: 3467  
Sequence: 1 gatcgcgacgaaggaatcc.....attgaataatcagatttct 3467

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## Descriptor

No.		Score	Query		DB	ID	Description
Result	Match		Length				
1	897.8	25.9	910	106	AL552687	AL552687	AL552687
2	809.8	23.4	865	106	AL575903	AL575903	AL575903
3	790	22.8	833	107	AU123737	AU123737	AU123737
4	753	21.7	913	154	BG470062	BG470062	BG470062
5	745.2	21.5	777	107	AU117503	AU117503	AU117503
6	740	20.8	903	152	BG328655	BG328655	BG328655
7	721.2	20.3	1031	141	BE877356	BE877356	BE877356
8	712.6	20.6	945	175	BG248713	BG248713	BG248713
9	710.8	20.5	739	107	AU124217	AU124217	AU124217
10	706.2	20.4	809	145	BE205938	BE205938	BE205938
11	705.8	20.4	732	107	AU118895	AU118895	AU118895
12	703.8	20.3	733	107	AU121341	AU121341	AU121341
13	694.8	20.0	934	175	BG251541	BG251541	BG251541
14	694	20.0	971	147	BF313923	BF313923	BF313923
15	690.2	19.9	765	108	AU144259	AU144259	AU144259
16	684.6	19.7	753	23	A1692928	A1692928	A1692928
17	683.8	19.7	784	153	BG386666	BG386666	BG386666
18	656.8	18.9	934	153	BE263281	BE263281	BE263281
19	652.8	18.8	740	175	BG289641	BG289641	BG289641
20	649.8	18.7	706	21	A1492151	A1492151	A1492151
21	647.2	18.7	790	147	BF314298	BF314298	BF314298
22	644.6	18.6	935	175	BG389785	BG389785	BG389785
23	640.2	18.5	671	166	BE314000	BE314000	BE314000
24	638.8	18.4	709	143	BF037033	BF037033	BF037033
25	638	18.4	765	165	BE298889	BE298889	BE298889
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27	637	18.4	886	152	BG38059	BG38059	BG38059
28	634.6	18.3	701	173	BG108197	BG108197	BG108197
29	634.2	18.3	660	117	AM516913	AM516913	AM516913
30	632	18.2	1062	175	BE359933	BE359933	BE359933
31	630.2	18.1	650	108	AU130535	AU130535	AU130535
32	627.8	18.1	671	108	AU134856	AU134856	AU134856
33	614.8	17.7	621	108	AU139193	AU139193	AU139193
34	610.4	17.6	781	165	BE297068	BE297068	BE297068
35	605.8	17.5	950	174	BE120237	BE120237	BE120237
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37	603.4	17.4	692	153	BE425507	BE425507	BE425507
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39	599.8	17.3	607	24	A1762627	A1762627	A1762627
40	593.4	17.1	783	153	BG424021	BG424021	BG424021
41	591.2	17.1	893	141	BE904713	BE904713	BE904713
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44	585.8	16.9	823	153	BG425233	BG425233	BG425233
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## ALIGNMENTS

[illegible]

RESULT	2
AL575903/c	
LOCUS	AL575903         865 bp     mRNA
DEFINITION	AL575903 LTI_NFLO06.PL2 Homo sapiens cDNA clone CSDBI067YH1.3 prime, mRNA sequence.
ACCESSION	AL575903
VERSION	AL575903.1    GI:12937524
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

BP 191 91006 EVRY cedex - France  
Email: [segrif@genoscope.cns.fr](mailto:segrif@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Location/Qualifiers  
1..865

BASE COUNT  
RCGIN

205 a 230 c 205 g 220 t 5 others

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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by a
division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : filangel@life tech.com URL :
http://fulllength.invitrogen.com"

```

Query Match	23.48	Score 809.8	DB 106	Length 865
Best Local Similarity	97.88	Pred. No. 7,2e-176		
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865	cccaagkgggggttaactttacacgccccagAACACAGATGTGTGGAGACCTGGCAA			806
2613	gcattctcatcacatcgtgttggcaaggtttaaacaaacaaacaaacaaacaa			2672
805	ggcatttcttatcaccatcgtgttggcaaaagttAAAAACAAAAAACCAAAAAA			746

[illegible]

RESULT	3						
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DEFINITION	AUI23737	833 bp	mRNA	EST	23-OCT-2000		
ACCESSION	AUI23737	NT2RM2	Homo sapiens cDNA clone	NT2RM200936	5'		mRNA
VERSION	AUI23737						
KEYWORDS	AUI23737.1	GI:10948453					
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	Homo sapiens						
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.						
AUTHORS	1 (bases 1 to 833)						
TITLE	Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,						
JOURNAL	Isogai,T., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and						
	HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S.,						
	Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki						
	Y., Sugano,S., Isogai,T.)						
	unpublished (2000)						





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Oy 1120 acatcagccctcaggaatgacccgctgtgtctcagccatccgttggttgaggct 1179
Db 182 ACATCATGCCCTTACGAATGACCGGTGTGTCTCCACCCATCCGTGTGTGGAGGCT 241
Oy 1180 ctgactacatcaatgacccgctcctcgtgtgtgtatagacagcagaagccactacta 1239
Db 242 CTGACTACATCAATGCCAGCTTCCTGGATGGTTATAGACACAGAGGCTTACATACCTA 301
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Oy 1300 ccacatcatcgtcactgctgacaaagctcggagagatggcagagagagaatgcccacagt 1359
Db 362 CCACCATCATGCTATGTGTGACAAAGCTTCGGAGATGGGAGGAGGAATAATGCCACACGT 421
Oy 1360 actgagcagcagagacgctctgctcgtctacagtaacttctgttgaaccgagtgagat 1419
Db 422 ACTGGCCAGCAGACGCGCTCTGCTCTGCTACAGTACTTGTGTGACCCGATGGCTGAGT 481
Oy 1420 acaaatgccccagtatatactcgtgagtcaagtcaaggtcagagatcccgagatggcagat 1479
Db 482 ACAACATGCCCCAGTATATCTGCTGAGTTCAAGGTCAAGGATGCCGCGGATGGGACAGT 541
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Db 542 CAAAGCAAAATCCGCGACCTTCAGTTCAAGACTGGCCAGAGCGAGCGGCGT 600
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Db 601 GCGAGGATTCATTGACTTCTATGCGGCAAGTGCATTAAGACCAAGAGCAG-7TGGACAGG 659
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Oy 1717 tgaagccctcgtgatac-cagcgtcctgtccatgtgtg-cagacagagagcagatcagct 1774
Db 780 TGAAGACCTGCTGACACAGCGCTCTGCATGGAGCGGCGAGACAGAACATGATCACT 839
Oy 1775 gtgctacgctgagccctgagtagtacctggcagcagctttgacacatatgca 1823
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RESULT 5
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LOCUS AUI17503 HEMBA1 Homo sapiens cdna clone HEMBA1001540 5', mRNA
DEFINITION AUI17503 HEMBA1 Homo sapiens cdna clone HEMBA1001540 5', mRNA
ACCESSION AUI17503
VERSION AUI17503.1 GI:10932475
KEYWORDS EST.
SOURCE EST.
ORGANISM Homo sapiens
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Oca,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute

```

TITLE  
JOURNAL  
COMMENT

```

1532-3 Yano, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project: 5'-6 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
source
location/Qualifiers
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/clone_lib="HEMBA1"
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/development="embryo, 10 weeks"
/note="Vector: pME18SFL3"
BASE COUNT 181 a 216 c 231 g 145 t 4 others
ORIGIN

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Best Local Similarity 98.8%; Pred. No. 5,4e-161;
Matches 769; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

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Oy 920 ggaagctgcacagctgagcagacagaggtgctgcgcgaactglatagccacatcca 979
Db 61 GGAGCGTCCACAGCTGCGGCGCACACAGAGTGTCTGCCACACCTGTATGCCACATCCA 120
Oy 980 gaagctggcacaagtgcctcagagagagagtgagcagcagcagcagcagcagcagcagc 1039
Db 121 GAAGCTGGGCGCAAGTCTCTCCAGGAGAGTGAACCGCCATGAGACTGGAATTCAAGTT 180
Oy 1040 gctggcagctcgaagggccacagcgtcccgctcctacagcgaacccgtgcgacaaga 1099
Db 181 GCTGGCCAGCTCCAGAGGCCACACAGTCCGCTTCAAGCCGCAACCTGTGCAACAA 240
Oy 1100 gttcaagaacccgctggtgaacatcagtcctcagagatgagcagcgtgtgtcagcgc 1159
Db 241 GTTCAAGAACCCGCTGCTGTAACATCATGCTCCACGAATGGAACCCGTGTGTGCAACC 300
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Db 301 CATCCGTGTGTGAGGGCTGTGACTATCATCATGCTCCAGCTTCTGGATGTATAGACA 360
Oy 1220 gaagaagcctacatagctacacagggcctctgagcagagagacagcagagactctggcg 1279
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Db 481 CAGGAGAAATGCCACAGTACTGCGCAGAGAGGCGCTGTGCTGTACAGTACTTGTGT 540
Oy 1400 tttgacccgagtgcagtagtacaacatgccccagtagtatctcgtgtgtgtcaaggttc 1459
Db 541 TGTGAGCCCGATGGCTGATGAACAATGCCCCAGTATATCTCGTGTGATTCAGAGTCAAC 600
Oy 1460 ggaagccggagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1519
Db 601 GGATGCCCGGAGTGGAGAGTCAAGAGCAATMGCGAGTT-CAGTTACAGACTGCGCAGAG 659
Oy 1520 gcagggcgtgcccagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1579
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Db	Accession	Source	Organism	Reference	Title	Journal	Comment
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Db	957	GenBank	Human	1031 bp			
Db	302	GenBank	Human	1031 bp			
Db	1017	GenBank	Human	1031 bp			
Db	362	GenBank	Human	1031 bp			
Db	1077	GenBank	Human	1031 bp			
Db	422	GenBank	Human	1031 bp			
Db	1137	GenBank	Human	1031 bp			
Db	482	GenBank	Human	1031 bp			
Db	1197	GenBank	Human	1031 bp			
Db	542	GenBank	Human	1031 bp			
Db	1257	GenBank	Human	1031 bp			
Db	602	GenBank	Human	1031 bp			
Db	1317	GenBank	Human	1031 bp			
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DB	422	TACTGGCCAGCAGAGCCCTCTGCTCTGCTACCACTTTGTGTGACCCGATGCTGAG	481
Db	1419	tacaacatgcccacaglatatctctgctgtaatctcaagtgcaagatgcccggatggcag	1478
Db	482	TACAACTATGCCCCAGTATATCTGCGGAGNCTTCAAGGTACCGATGCCGGATGGGAG	541
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Db	542	TCAAGGACAAATCCGGCAGTTCAGGTTCCAGTTCACAGACTGGCCAGACGAGCGGTGCCAAGACA	601
Qy	1539	ggcgaaggatctatgtacttcaatcagcgagcaggtgcataaagacaagaagagcaatgttgacag	1598
Db	602	GCGAGGAGCATTCATTGTGACTTCACTGGGGGACAGTGCTCAATAGAC--AAGAACAGTTTGGACAG	659
Qy	1599	gagcgagccatcaccaggtgacgcgcagctgtctgagcgtggagccgacac--ggagtgatcatcac	1657
Db	660	GATGGGCTATACAGGGGTGACAGTGCAGAGTGTGCTGGCGGGCCGACCGGGGGTTCATCAC	719
Qy	1658	tctgagcatcgtctctggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	1717
Db	720	TCTGAGCAATCGTCTGAGCCGATG--GCTATGAAAGCG--GGCAGACATGTTACAGAACCGT	777
Qy	1718	gaagaccctcggttacaacagcgtctgcatatgtgcagacagagagaccagtcacgtgtg	1777
Db	778	GA--AACTGCTTAAACACGCTGTGCGC--TTGGGCGACACACAGACAGACAGATTCCTGTGTA	833
Qy	1778	c 1778	
Db	834	C 834	
RESULT	9		
LOCUS	AU124217		
DEFINITION	AU124217 NT2RM2 Homo sapiens CDNA clone NT2RM2001847 5', mRNA		
ACCESSION	AU124217		
VERSION	AU124217.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 739) Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and Isogai,T.		
TITLE	HRI human CDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S., Isogai,T.) Unpublished (2000)		
JOURNAL	Genomics Laboratory		
COMMENT	Helix Research Institute 1532-3 Yama, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3951 Fax: 81-438-52-3952 Email: genomics@hri.co.jp HRI human CDNA project: 5'- & 3'-end one pass sequencing: Helix Research Institute; CDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute. Location/Qualifiers 1..739 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="NT2RM2001847" /clone_1id="NT2RM2" /cell_type="teratocarcinoma" /cell_line="NT2" /note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal precursor cells"		

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Best Local Similarity		98.4%	Pred. No. 4.5e-153:		
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Gaps					
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1	CATCAATGCAACTACATCATGATGGCTACCGGACGACAAATAGCTTACATGGCCACGAGG				60
380	ccccctgcgcgagacatgagcagatcttcctcggaaatggtgttgaaacgcgcagccac				439
61	CCCCCTGCCCGAGACCATGGCCATTCTCTGAGAAATGGTGTGGAAACACGACGCGCCAC				120
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121	TtGtGtCATGATGTGACACGCGCTGGAGGAGAGTCCCGGTAATAATGATCATCTACTGGCC				180
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181	AGCCCGTGGACCGAGACCTGTGGCTTATTCAGGTGACCCGTTGGACACAGTGGAGCT				240
560	ggccaatacactgtgtgcacaccttcgcacatcccaagaagtgtcctcagtggaagaagcga				619
241	GGCCACATATACACTGTGGCGCACTTCGCATCCCAAGAGTGGCTCACTAGTGAAGAGCTTGA				300
620	gctgcctcagtttcagttatagttcctggccgagacacatgagttcctgtatcccaactcc				679
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680	catcttgacccttctacagacgggtcaagagcctgcgaaccccttagacgagagggcccatggtc				739
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421	GGTGCACTGACACCGGCGGTGTGGCGCACCGCGCTGTCTTACGTGATGTATGTCATGTGT				480
800	ggaagcgaatgaagaacggaagaacggttgacatctatgagcaagtgacgtgcacatgacatc				859
481	GGAGCGGATGAAGACGAGAGAAGACGGTGGACATCTATGTCGACGTGACCTGCATGCGATC				540
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601	TGGAGGCTGCCACGTCGCGGACACAGAGGTGCTGCCCAACTGTATGCCCAATGAC				660
979	agaagcttgggcaaggtgctctccaggggaagtgatgacggcgaatggaactcgaatctcaagt				1038
661	AGAAGCTTGCGCAAGTGCCTTTCAGAGGAGANTGTGACCGNCATGAGAGCTCGAGTTCAAT				720
1039	tgtctggcgaagctccaagg 1056				
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LOCUS	BF205938				
DEFINITION	BF205938: 809 bp mRNA				
ACCESSION	601869567F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4098064				
VERSION	BF205938				
KEYWORDS	EST				
SOURCE	human				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				



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Oy 705 aagagcctgacacccctctagaagcagagccatggtggtgtagctgacgagcggtggc 764
Db 181 AAGGCTGCAACCCCTAGACGAGGCGCCATGCTGTGCTCACTGACGCGCGGCTGGCC 240
Oy 765 cgcagcgtgctctcctcgtgtagttagtgcattgtggagcgagatgaagcagaagagc 824
Db 241 CGCAGCGGCTGCTTCAATGCTGATGATGTCATGTCATGTCATGTCATGTCATGTCATGTC 300
Oy 825 gtggacatctatgagcagcgtgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgt 884
Db 301 GTGGACATCTATGCGCACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 360
Oy 885 gagagcagtaagtgctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 944
Db 361 GAGGACCATGACCTGCTTCATCATCATGAGCGCTGCTGAGGCTGCTGAGGCTGCTGAGGCT 420
Oy 945 gaggtgctgctcgcagacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgt 1004
Db 421 GAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
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Db 481 GAGAGTGAGACCCGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 540
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Oy 1244 ggggacctctggc 1255
Db 721 NGGCGCTTTGGC 732

RESULT 12
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DEFINITION AU121341 HEMBI Homo sapiens cDNA clone HEMBI1002629 5', mRNA
ACCESSION AU121341
VERSION AU121341.1 GI:10936576
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 733)
AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
Isoqal, T.
HRI human cDNA project
Unpublished (2000)
Contact: Takao Isoqal
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp

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Matches 705; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Oy 724 acgagagggcccatggtggtgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgt 783
Db 61 ACGAGGCGCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Oy 784 tgattgatgcatgttggagcgatggaagcagagagagagagagagagagagagagagagagag 843
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Oy 844 tgactgtatgcatgacacagagagagagagagagagagagagagagagagagagagagagag 903
Db 181 TGACTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
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Db 241 TCCATGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
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Oy 1084 acctcctcctgcaacaagtctcagagacggtgtagacatcctgctcctcctcctcctcctcct 1143
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Oy 1324 agcttcgagagagagagagagagagagagagagagagagagagagagagagagagagagag 1372
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RESULT 13
LOCUS BG251541 934 bp mRNA EST 13-FEB-2001

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DEFINITION 602363412F1 NIH\_MGC\_90 Homo sapiens cDNA clone IMAGE:4471731 5', mRNA sequence.

ACCESSION BG251541

VERSION BG251541.1 GI:12761357

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 934)

AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D. Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov) Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov> Plate: LAM10291 row: h column: 04 High quality sequence stop: 794.

FEATURES

Source 1..934

Location/Qualifiers

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/clone="IMAGE:4471731"

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/tissue\_type="adenocarcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: liver; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC library."

BASE COUNT 173 a 286 c 291 g 184 t

ORIGIN

Query Match 20.0%; Score 694.8; DB 175; Length 934; Best Local Similarity 94.2%; Pred. No. 2.3e-149; Matches 754; Conservative 0; Mismatches 42; Indels 4; Gaps 3;

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DB 61 TGTTTGTGACCCGATGGCTGAGTACAAACATGCCCCAGTATATCTCTCGTGAAGGT 120

QY 1457 cgcgagtcgcggagatgagtcagtaagaagaacatccggcaggtccagttcagagactggcc 1516

DB 121 CACGGATGCCCGGAGTGGCACTCAAGACAAATCCGGCAATTCACATTCACAGACTGGCC 180

QY 1517 aagagcagggcgatgcccagaagacagcgagggatcattcattcattcagggcaggtgcatata 1576

DB 181 AGAGCAGGGCGTGCACCAAGAGCGAGGATTCATTGACTTCATCAGGCGAGTGCATTA 240

QY 1577 gaccaaaggagcagtttgagcagagatgagcctatacagtgatcagtgatgagtgag 1636

DB 241 GACCAAGGAGCAAGTTGGACAGAGATGGCCCTATCAAGGTCGACACTGCAGTGGCTGG 300

QY 1637 ccgcacacggaggtgtcatcactctgagcactgctccgtgagcgatgctatgaggggt 1696

DB 301 CCGCACCGGGGCTTTCATCTGAGCATCTGCTCCGAGCGCATGCGCTATGAGGCGCT 360

QY 1697 ggtcgaacatgtttcagacacgtgaagacccctgctacacagcgttccctgcatggtgagac 1756

DB 361 GGTGCAATGTTTCAACACCGTGAAGACCTGCGTACACAGCTCCGTCATGATGAGAC 420

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DB 421 AGAGCAGCAATACAGCTGTGTACCGTCCGGCCCTGAGTACCTCGCAGGCTTTGACCA 480

QY 1817 ctatgcaacgtactactacgcctccctctctccgcacaccccgcggtgggtcggagag 1876

DB 481 CTATGCAACGTAACTACCTCCCTCTCTCCGACACCCCGCTCGGGGCTCCGGAGG 540

QY 1877 ggaaccagctctctgagcagatcacagacatgcttcagccctccacagatgtctgta 1936

DB 541 GACACCACTCTCTGTAGCATACCAATGTCATGACCTCTCTTCAAGCATGCTGTGA 600

QY 1937 ctgcgacagacagccacagggagatcacagcgtttcagaagacttgcacacacaga 1996

DB 601 CTGCGACAGCACAGCCACGCGGAGATCACAGCGTTTGAAGAGTTGCCACACAAATCAG 660

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DB 661 AGAGCCTAGAACATCTCTGGCAAGTGAGAG--CCAGTAGCAGGCACTGTGG-CTTCTG 718

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RESULT 14

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LOCUS 601900545F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:4129642 5', mRNA sequence.

DEFINITION BF313923

ACCESSION BF313923.1 GI:11262008

VERSION BF313923

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 971)

AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D. Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov) Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov) Plate: LCM1024 row: j column: 11 High quality sequence stop: 661.

FEATURES

Source 1..971

Location/Qualifiers

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/db\_xref="taxon:9606"

/clone="IMAGE:4129642"

/clone\_11b="NIH\_MGC\_19"

/tissue\_type="neuroblastoma"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: brain; Vector: pORF7; Site: 1: XhoI; Site: 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC library."

BASE COUNT 210 a 298 c 301 g 161 t 1 others

ORIGIN



||||| 1760

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Db 662 GACCACTATCANCCTTGTGCTACCCGCTGCGGGCTGAGTACCTTGGGCACTTTGACCA 721  
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Search completed: August 21, 2001, 19:06:02  
Job time: 2890 sec

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Y00815.1 GI:34266		
antigen; cell surface glycoprotein; glycoprotein; immunoglobulin superfamily; LAR gene; leukocyte common antigen; neural cell adhesion molecule; transmembrane protein.		
human.		
Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
1 (bases 1 to 7702)		
Salto, H.		
Direct Submission		
Submitted (15-SEP-1988) Salto H., Dana-Farber Cancer Institute, 44		
Binney Street, Boston, MA 02115		
2 (bases 1 to 7702)		
Streuli, M., Krueger, N.X., Hall, L.R., Schlossman, S.F. and Salto, H.		
A new member of the immunoglobulin superfamily that has a cytoplasmic region homologous to the leukocyte common antigen		
J. Exp. Med. 168 (3), 1523-1530 (1988)		
3 (bases 1 to 7702)		
Schappaveld, R.O., van den Maadenberg, A.M., Schepens, J.T., Weghuis, D.O., Geurts van Kessel, A., Wieringa, B. and Hendriks, W.J.		
The mouse gene P1pif encoding the leukocyte common antigen-related molecule LAR: cloning, characterization, and chromosomal localization		

JOURNAL MEDLINE FEATURES	Genomics 953944448	Location/Qualifiers
source	27 (1), 124-130 (1995)	1..7702
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Oy	245	ctatgcaaatgcatatcgctctaacgcaactctccagatctccttaacctctatgtagcgt	304
Db	4480	CTATGCAAAATGTCATGCGCTACGACCACTCTCGAGTCACTCTTAACCTTATCGATGGCGT	4539
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Db	4600	CATCGCAACGACAGGGCCCCCTGCCGAGACCAATGGCGATTCTTGGAAGATGCTGGGA	4659
Oy	425	acagcgcaacgcccactgtgtgtcatatgatagacaagcttggagagaagtctccggttaaatg	484
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Oy	545	ggaacacagttagagcttgcscacataacatltgtgcaccttgcacatccaaagagtgctc	604
Db	4780	GGACACAGTGGAGTGGCCACATACATAGTGGCGACCTTGCACTGCACMAAGATGGCTC	4839
Oy	605	caatgagaaagcgtagagctctgcttcaagttctcaatctgacctggccaagacatgaaatctc	664
Db	4840	CAGTGAAGAAAGCTGAAGCTGACCTCAAGTTTCAGTTCAATGAGGCTTGCCAGACCAATGGAGTTCC	4899
Oy	665	tgaatcaacaaactccatctctgagcctctccaaagcagcggtcgaagcgctcaaacccctaga	724
Db	4900	TGAGTACCAACCACTCCATCTCGGCTTCTTAGAGCGGTCAAGGCTGCMAACCCCTAGA	4959
Oy	725	cgcaagggcccaatgtgtgtgtaacctggacgacggcggttgggcgcaacggctgcttcatcgt	784
Db	4960	CGCAGGGCCCAATGTGTGTGTAACCTGGACGACGGCGGTGGGCCCCACCGGCTCTTCAATCGT	5019
Oy	785	gatttgaatgcattgtcttgagcagcgtatgaacacagaaagagtgatgacatctatgtgccagt	844
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Oy	845	gacctgcaatgtgataccaaagggaaatacaatgtgtcagaacggaagagacagtagctgttcat	904
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Oy	965	gtatgcccacatccagaagcttggcccaagtgtcctccagggagagtgtgaacgcctatga	1024
Db	5200	GTAATGCCCAATCCAAAGACTGGGCCMAATGTGCTCCAGGGGAGAGTGTGACCCCAATGGA	5259
Oy	1025	gtctgaatctcaagtgtctgtggcagactctcaagggcccaacgctcccgctctatacggccaa	1084
Db	5260	GCTCGAATTCAAATGTTCTGTGGCAGGCTCCAAAGGCCCAACGTCGCCGCTTCAATCAGCCCA	5319
Oy	1085	ccgtgcccctgtaaaagttcaagaagacggcctgtgtgaacatactgcccctcaatgtgacccg	1144
Db	5320	CGTGGCCCTGCACAAAGTTCAAAACACGGGCTGTGTAAACATCATGCCCAAGAAATTGACCG	5379
Oy	1145	tgtgtgtcttgcagcccatctcgtgtgtgtgagggtctgcatatactaaatgccaagcttccct	1204
Db	5380	TGTGTGTCTGCAAGCCATCCGtGtGTGTGAGGCTTGACATCAATCAATGACCAAGCTTCTT	5439

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Db	5440	GGATGGTTATATACACAGACAGAAAGGCGCTACATAGCTACACAGAGGCGCTCTGGCACAGACAC	54
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QY	1325	gcttcgggagatgaggcagaaggagaaatgcccacgaactctggccggcagagcgtctgctcg	13
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QY	1385	ctaccaggaactctgtttgttagcccgatgagctctgagtaacaatgccccagtatatccctg	14
Db	5620	CTACCAAGTACTTGTATTGTTACCCGAGGCGCTGAGTCAACATGCCCCCATATATCTCTCG	56
QY	1445	tgaatctcaagaatccacgagatcccccggatgaggcagttaaagaacatccggcagttccagtt	15
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QY	1805	cagactctgacccactatgaacagtaactacgcgtccctccctccctccgcacaccccccgcgtg	18
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Db	6100	GGGCTCCGAGGAGGCCAGGCTCCTCTAGGCATACCGACCATGTCTACGCCCTCTCTAGG	61
QY	1925	cgaatgctgtctactgycgacagagacagcccacgggatatcaaacgcttctcagaaacgttgc	19
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QY	2045	gtgggcctctctgctcacacagaccacccctggagcccgtctcaagctctctgtttgctctcc	21
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QY	2105	gaattctcctcattctctctcatgagggtggggttggggcgaagccctctttaaatacat	21
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QY	2165	taagtgagggtatgacttgaggagatttaagcctctccctctgattcttctctctccctcgaatcc	22
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QY	2225	gtacctgcagaatggggccacatctagaagggttggggttaattgcttctctctctcttctt	22
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QY	2285	tttgtatgactctctgctgaaggacaaacattgctctctctctctgctcaaaagctctgaaagctc	23

Db	7600	GTAGAGTTCAGCTGTTGTACACAGTCTGTTCTTCTATTCTTTAGAAAACTACAGCATCAT	7659
Oy	3425	tgcaaatcttgatgtaataaattgaaataacagattct	3467
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RESULT	2
LOCUS	M60103
DEFINITION	Rattus norvegicus leukocyte common antigen related protein mRNA, 3'
ACCESSION	M60103
VERSION	60103.1
KEYWORDS	GI:205130
SOURCE	leukocyte common antigen related protein.
ORGANISM	Rattus norvegicus adult hypothalamus, CDNA to mRNA.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
AUTHORS	1 (sites)
TITLE	Struill, M., Krueger, N.X., Hall, L.R., Schlossman, S.F. and Salto, H. A new member of the immunoglobulin superfamily that has a cytoplasmic region homologous to the leukocyte common antigen
JOURNAL	J Exp. Med. 168, 1523-1530 (1988)
REFERENCE	89035978
AUTHORS	2 (bases 1 to 4190)
TITLE	Cloning, bacterial expression, purification and characterization of the cytoplasmic domain of rat LAR, a receptor-like protein tyrosine phosphatase
JOURNAL	J Biol. Chem. 266, 19688-19696 (1991)
REFERENCE	92011772
JOURNAL	Location/Qualifiers
MEDLINE	1. 4190
FEATURES	/organism="Rattus norvegicus"
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BASE COUNT	942 a	1167 c	1351 g	930 t
ORIGIN				

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Matches 2927	Conservative	0	Mismatches	474	Indels	77	Gaps	23

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Db	771	CGGCTGAAGAGCTCCCTGTTGGCCACTCTTCTACCTGTGGAAATGCGAAGCCTTA	830

9	1588.6	45.8	5723	94	AF300943	Mus muscu
10	1546.6	44.6	2213	95	U00477	U00477 Rattus norv
11	1505	43.4	1638	54	G06614	G06614 human STS M
12	1285	37.1	4773	97	HSU41725	U41725 Human prote
13	1285	37.1	6000	9	AR031690	AR031690 Sequence
14	1285	37.1	6000	10	161404	I61404 Sequence 6
15	1285	37.1	6000	57	HSU40317	U40317 Human prote
16	1281	36.9	5978	94	MMPTPN03	X82288 M. musculus
17	1277.4	36.8	5383	95	RATLARPTP	L12329 Rat leukocy
18	1277.4	36.8	6469	95	RATLARPTP	L12329 Rat leukocy
19	1276.4	36.8	4724	95	RATLARPTP	L19933 Rattus norv
20	1273.2	36.7	5690	9	AR060681	AR060681 Sequence
21	1273.2	36.7	5690	9	AR064169	U35234 Human prote
22	1256.2	36.2	6363	97	HSU35234	D28530 Mouse mRNA
23	1256.2	35.3	6734	94	MMPTPN03	L19180 Rat recepto
24	1234.2	35.3	5412	95	RATPTP1	AF197945 Xenopus 1
25	1218.4	35.1	7297	8	AF197945	L32780 Gallus gall
26	1170.6	33.8	4613	8	CHKCRYP	L38929 Homo sapien
27	1095.8	31.6	6263	97	HMPPTP	X54133 Human Hprt
28	1094.6	31.6	4584	93	HSPPTP	AF198450 Xenopus 1
29	1074.8	30.6	4584	93	HSPPTP	AF197944 Xenopus 1
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33	970	28.0	1029	9	AX000414	M27700 D. melanog
34	952.6	27.5	1669	4	AB033566	AB033566 Branchios
35	939.6	27.1	1669	4	AB033566	AB033566 Branchios
36	919	26.5	1517	8	AB033581	AB033581 Potamo
37	919	26.5	1517	8	AB033581	AB033581 Potamo
38	914.4	26.4	1517	8	AB033581	AB033581 Potamo
39	868.4	25.0	1851	8	AB033569	AB033569 Bptactretu
40	850.8	24.5	1616	8	AB033571	AB033571 Eptactretu
41	841.6	24.3	1878	8	AB033571	U03273 Rattus norv
42	830.8	24.0	1194	95	AF017084	AF017084 Hirudo me
43	818.4	23.6	4314	5	AF017084	U36857 Drosophila
44	796	23.0	6227	5	AF017084	
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## ALIGNMENTS

RESULT	1	ALIGNMENTS
LOCUS	7702 bp mRNA	19-SEP-1995
DEFINITION	Human mRNA for LCA-homolog. LAR protein (leukocyte antigen related).	
ACCESSION	Y00815.1	GI:34266
VERSION	Y00815.1	GI:34266
KEYWORDS	antigen; cell surface glycoprotein; glycoprotein; immunoglobulin superfamily; LAR gene; leukocyte common antigen; neural cell adhesion molecule; transmembrane protein.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS	Saito, H.	
JOURNAL	Submitted (15-SEP-1988) Saito H., Dana-Farber Cancer Institute, 44 Binney Street, Boston, MA 02115	
REFERENCE	2 (bases 1 to 7702)	
AUTHORS	Streuli, M., Krueger, N.X., Hall, L.R., Schlossman, S.F., and Saito, H.	
TITLE	A new member of the immunoglobulin superfamily that has a cytoplasmic region homologous to the leukocyte common antigen	
JOURNAL	J Exp. Med. 168 (5), 1523-1530 (1988)	
MEDLINE	89035978	
REFERENCE	3 (bases 1 to 7702)	
AUTHORS	Schappaveld, R.O., van den Maagdenberg, A.M., Schepens, J.T., Meghuis, D.O., Geurts van Kessel, A., Kiering, B., and Hendriks, W.J.	
TITLE	The mouse gene P19f encoding the leukocyte common antigen-related molecule LAR: cloning, characterization, and chromosomal localization	

JOURNAL	Genomics 27 (1), 124-130 (1995)
MEDLINE	95394448
FEATURES	
source	Location/Qualifiers
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DEFINITION	Rattus norvegicus leukocyte common antigen related protein mRNA, 3		
ACCESSION	M60103		
VERSION	M60103.1	GI:205130	
KEYWORDS	leukocyte common antigen related protein.		
SOURCE	Rattus norvegicus adult hypothalamus, CDNA to mRNA.		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine;		
REFERENCE	1 (Stiles)		
AUTHORS	Streuli,M., Krueger,N.X., Hall,L.R., Schlossman,S.F. and Saito,H.		
TITLE	A new member of the immunoglobulin superfamily that has a cytoplasmic region homologous to the leukocyte common antigen		
JOURNAL	J. Exp. Med. 168, 1523-1530 (1988)		
REFERENCE	2 (bases 1 to 4190)		
AUTHORS	Poc.D.A., Woodford,T.A., Remboutsika,E., Haun,R.S. and Dixon,J.E.		
TITLE	Cloning, bacterial expression, purification and characterization of the cytoplasmic domain of rat LAR, a receptor-like protein tyrosine phosphatase		
JOURNAL	J. Biol. Chem. 266, 19688-19696 (1991)		
MEDLINE	92011772		
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Best Local Similarity	84.2%	Pred. No. 0;	
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Db	771	CGGCGCTAAGAGACTCCCTCTTGCCACACTCTTGTACACCTCTGGAAGATTCGAAGCTTAA	870



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2001, 18:19:42 ; Search time 4532.97 seconds  
(without alignments)  
11830.364 Million cell updates/sec

Title: US-09-719-272-1

Perfect score: 3467

Sequence: 1 gatacgcgactgaagactcc.....attgaataatcagattctt 3467

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: gb\_in3:\*  
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95: gb\_pi11:\*  
96: gb\_pi12:\*  
97: gb\_pi13:\*  
98: em\_ba3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	2335.6	67.4	4190	94	M60103
3	1917.2	55.3	6545	95	M60103 Rat
4	1876.8	54.1	4685	95	RATLARR
5	1694.6	48.9	2202	94	RATLARR
6	1668.2	48.1	3941	95	RATLARR
7	1657.8	47.8	152891	62	AC011772
8	1656.8	47.8	128327	79	AL158083



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DB 4360 CATCGAGCGCCCTCAAGGCCAACGATGGCTCTCAAGTTCTCCAGAGATATGATCCATGCA 4419  
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REFERENCE	AUTHORS	TITLE
1 (sites)	Steuil, M., Krueger, N. X., Hall, L. R., Schlossman, S. F. and Saito, H	A new member of the immunoglobulin superfamily that has a cytoplasmic region homologous to the leukocyte common antigen
	J. Exp. Med. 168, 1523-1530 (1988)	
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TITLE  
Cloning, bacterial expression, purification and characterization of the cytoplasmic domain of rat LAR, a receptor-like protein tyrosine phosphatase  
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MOL. CELL. BIOL.  
MEDLINE  
J. Biol. Chem. 265, 19688-19696 (1991)  
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 Zhang, J.S. and Longo, F.M.  
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 J. Cell Biol. 128 (3), 415-431 (1995)  
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 Zhang, J.S.  
 Direct Submission  
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 152891)

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# AUTHORS TITLE JOURNAL REFERENCE AUTHORS

Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
Homo sapiens chromosome 15, clone RP11-134C3  
Unpublished  
2 (bases 1 to 152891)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,  
Brown, A., Castle, A., Collins, R., Collins, S., Collins, S., Collins, S.,  
Cooke, P., DeBartolo, K., Dewar, K., Dominko, M., Donnell, L., Doyle, M.,  
Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Horton, L.,  
Howland, J., Jorde, L., Jones, C., Kamm, B., Keane, A., Klein, J.,  
Lehoczky, J., Liu, C., Locke, K., MacDonald, P., Marquis, N.,  
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J.,  
Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,  
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Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
Testa, S., Tjelle, A., Vassiliou, H., Vo, A., Wheeler, J., Wu, X.,  
Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (14-OCT-1999) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Feb 28, 2000 this sequence version replaced g1:630598.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

## COMMENT

## TITLE JOURNAL

Center: Whitehead Institute/ MIT Center for Genome Research  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
Project Information  
Center project name: 134.C.3  
Center clone name: 134.C.3

Summary Statistics  
Sequencing vector: M13, M7815: 100% of reads  
Chemistry: Dye-terminator Big Dye: 100% of reads  
Assembly program: Phrap: version 0.960731  
Consensus quality: 128435 bases at least 400  
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Insert size: 151291: sum-of-ctg  
Quality coverage: 4.2 in 020 bases: agarose-fp  
Quality coverage: 4.4 in 020 bases: sum-of-ctgs

NOTE: This is a 'working draft' sequence. It currently  
\* consists of 17 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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Quality coverage: 4.76x in Q20 bases; sum-of-ctrls quality
coverage: 4.26x in Q20 bases; agarose-ftp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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Matches 1703; Conservative 0; Mismatches 3; Indels 25; Gaps 2;

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AUTHORS	1 (bases 1 to 5723)				
TITLE	Kistelow,P. and Terszowski,G.				
JOURNAL	LAR cDNA sequence from mouse thymus				
REFERENCE	Unpublished				
AUTHORS	2 (bases 1 to 5723)				
TITLE	Kistelow,P. and Terszowski,G.				
JOURNAL	Direct Submission				
FEATURES	Submitted (29-AUG-2000) 048, Basel Institute for Immunology,				
source	Grenzacherstrasse 487, Basel, BS 4005, Switzerland				
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gene  
CDS

gene

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 4773)
Endo,N., Rutledge,S.J., Opas,E.E., Vogel,R., Rodan,G.A. and
Schmidt,A.
Human protein tyrosine phosphatase-sigma: Alternative splicing and
inhibition by biophosphates
J. Bone Miner. Res. (1995) In press
2 (bases 1 to 4773)
Endo,N., Rutledge,S.J., Opas,E.E., Vogel,R., Rodan,G.A. and
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Direct Submission
Submitted (30-NOV-1995) Jeff Aaronson, Bioinformatics, Merck & Co.,
Inc., PO Box 2000, MS R80A-1, 126 E. Lincoln Ave., Rahway, NJ
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Db	4798	CTACATGTGTGACAGCGGAGCCAGTACACTTCATCCATCAGAGGCCCTCTGGAAGCGGT	485
Oy	929	cacgtgcgacacagaagtgtacctgcccgaacacctgatgcccacatacccaagaagctgg	988
Db	4858	GGGCTGTGGCAACACAGAAATGTCGCCGACGACACCTCTATTGCCATTCAACAAACTGCG	491
Oy	989	ccaagtgtcctcaggggagagtgtgaacgcgcatgagagctcagatctaaagtctgtgcag	1048
Db	4918	CGAGTGTGAGCTGTGGCCAAACGTCATCTGATGGAATCGAATCGAATTCAGCGGTGCTAA	497
Oy	1049	ctcaagaagcccaacagctcccggtctaatctgacgcaaacctgcgacctcaacaagttaagaa	1108
Db	4978	CTCCAAAGCCCAACGTCAGACGCTTCATCATGTCGCAATTCGCTTTTAAGAAATTCAGAA	503
Oy	1109	ccgagctgtgaaacatactgacctgaatgaaatgaaacggctgtgtctctgaagccataccgtg	1168
Db	5038	CCGCGCTGTGAACATCATGTGCTTATGAGAGCAACAGGGGTCTGTGCAACCATTCGGGG	509
Oy	1169	tgtgtagaggtctgacatacctaattgcaagcttctctgtatgttataagacaagaagc	1228
Db	5098	TGTGAGAGGCTTGTACATCAACACCCAGCTTCATTGTATGGCTACACAGCGACGAAGAGC	515
Oy	1229	ctacatagtctacaaggggctctctgcaagaagacgcaagactcttggcacatgata	1288
Db	5158	CTACATGTGCACACAGGGGCCGCTGGCGGAGACACAGGAAGACTTTCTGGCCATGCTGTG	521



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Db 4138 ACATTCCAAACCTGGAAGTGAACAAGCCGAAGAACCGCTATGCTCCATATGA 4197
Oy 269 GCACCTGAGTGCATCCTTACCTTACATGAGTCCCGGAGGTAACATCAATGC 328
Db 4199 CCACCTCCGCTGATCTCCACAGCCATTGAAGCCATATGGGACATGATATCAATGC 4257
Oy 339 CAATACATCAGATGATCCGCAAGATGCTTACATGCAAGCAAGAGGCCCCCTGC 388
Db 4258 CAATACCTGAGACGGCTACCGGCTCAGAAAGCCTACATTCGCCAGGAGGCGCTGCC 4317
Oy 389 CAGAGACATGAGCAATCTTCGAGAAATGATGAGGAAAGCAAGCAAGCAAGTATGCAT 448
Db 4318 TGAGACCTTGTGGGACTTCTTGCGATGATGAGGACACGCTCGGACATCTGCAT 4377
Oy 449 GATGACAGCTGAGGAGGAGAGTCCCGTGAATGATGATGATGATGATGATGATGATG 508
Db 4378 GATGACAGCTGAGGAGGAGAGTCCCGTGAATGATGATGATGATGATGATGATGATG 4437
Oy 509 CACGAGACCTGAGTGCATCTTACATGAGTGCATGATGATGATGATGATGATGATGATG 568
Db 4438 CACGAGACCTGAGTGCATCTTACATGAGTGCATGATGATGATGATGATGATGATGATG 4497
Oy 569 CACTGAGCACTGAGTGCATCTTACATGAGTGCATGATGATGATGATGATGATGATGATG 628
Db 4498 CTGCGTGAAGACATCTTCTGCAACAAGATGCTCAGATGATGATGATGATGATGATG 4557
Oy 629 GTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 688
Db 4558 GTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4617
Oy 689 CTCTCAAGCAAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 748
Db 4618 TTTCCTCCGAGAGTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 4677
Oy 749 CAGCGAGGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 808
Db 4678 CAGCGAGGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4737
Oy 809 GAAGCAAGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 868
Db 4738 CAAGCCAGAGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4797
Oy 869 CTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 928
Db 4798 CTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4857
Oy 929 CAGCTGAGGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 988
Db 4858 GAGCTGAGGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4917
Oy 989 CAGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1048
Db 4918 CAGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4977
Oy 1049 CTCCAGAGGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1108
Db 4978 CTCCAGAGGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5037
Oy 1109 CAGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1168
Db 5038 CAGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5097
Oy 1169 TGTGAGGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1228
Db 5098 TGTGAGGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5157
Oy 1229 CTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1288
Db 5158 CTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5217
Oy 1289 GAGAGCAATCTCCATCATGATGATGATGATGATGATGATGATGATGATGATGATG 1348

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Db 5218 GGAGAACATTCAGAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 5277
Oy 1349 ATGCCAGTACTGAGCAAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1408
Db 5278 GTGTACACAGTACTGAGCAAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5337
Oy 1409 GATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1468
Db 5338 GATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5397
Oy 1469 GATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1528
Db 5398 GATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5457
Oy 1529 GATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1588
Db 5458 GATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5517
Oy 1589 GATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1648
Db 5518 GATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5577
Oy 1649 GATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1708
Db 5578 GATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5637
Oy 1709 GATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1768
Db 5638 GATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5697
Oy 1769 GATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1828
Db 5698 GATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5757
Oy 1829 GATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1888
Db 5758 GATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5817

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